

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 07:16:51 ; Search time 6492 Seconds

(without alignments)
200.291 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KXSLPHDYRSATEPYISQINLIXYTX 30

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
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-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	1859	8 AF031478	AF031478 Candida a
2	107	73.8	2332	8 CSMNSOD	Y11598 Candida sp.
3	103	71.0	621	6 AR257498	AR257498 Sequence
4	103	71.0	735	1 NAU02341	U02341 Nocardiella as
5	101	69.7	657	1 AF333434	AF333434 Mycobacte
6	101	69.7	900	6 AX708734	AX708734 Sequence
7	101	69.7	960	1 MAU11550	U11550 Mycobacteri
8	101	69.7	1741	1 AF180816	AF180816 Mycobacte
9	100	69.0	815	1 D13288	D13288 Mycobacteri
10	100	69.0	908	11 CNS06105	AL400539 T3 end of
11	100	69.0	2045	8 SCSDMMNG	X02156 Yeast gene
12	100	69.0	18715	8 YSCHL2825	U10400 Saccharomyc
13	100	69.0	24431	8 YSCH9780	U0555 Saccharomyc
14	99	68.3	1071	1 AF061031	AF061031 Mycobacte
15	99	68.3	1478	1 MFSODA	X70924 M.fortitum
16	98	67.6	649	1 MLEP8OD	X16453 Mycobacteri
17	98	67.6	344050	1 MLEP8OD	AL583917 Mycobacte
18	94	64.8	790	1 MTSOD	X2861 M. tuberculosis
19	94	64.8	943	1 AF077406	AF077406 Mycobacte
20	94	64.8	1321	1 AF061030	AF061030 Mycobacte
21	94	64.8	1321	6 AX708732	AX708732 Sequence
22	94	64.8	14282	1 AE007188	AE007188 Mycobacte
23	94	64.8	244800	1 BX842584	BX842584 Mycobacte
24	94	64.8	278492	1 BX248347	BX248347 Mycobacte
25	91	62.8	567	1 PFSOD	X91650 P.firrendure
26	91	62.8	567	1 PFSOD	Y09012 P.firrendure
27	84	57.9	302529	1 AE016851	AE016851 Triopherym
28	82	56.6	239050	1 BX251411	BX251411 Triopherym
29	80	55.2	655	3 AB079877	AB079877 Maripheya
30	80	55.2	954	4 AB001693	AB001693 Equus cab
31	80	55.2	4439	1 GSP312188	AJ312188 Gordonia
32	79	54.5	812	6 E15569	E15569 CDNA encodi
33	79	54.5	812	6 AR222758	AR222758 Sequence
34	78	53.8	429	3 AY211085	AY211085 Farfante
35	78	53.8	349659	1 BX248360	BX248360 Coryneb
36	77	53.1	600	6 AX123311	AX123311 Sequence
37	77	53.1	606	6 BD165428	BD165428 Novel pol
38	77	53.1	606	4 RABMSD	L28608 Oryctolagus
39	77	53.1	960	1 AB055218	AB055218 Coryneb
40	77	53.1	1143	6 AR338437	AR338437 Sequence
41	77	53.1	1143	6 AX136077	AX136077 Sequence
42	77	53.1	1143	6 BD011434	BD011434 DNA, amin
43	77	53.1	2207	1 AF236111	AF236111 Coryneb
44	77	53.1	302070	1 AP005223	AP005223 Coryneb
45	77	53.1	309400	6 AX127153	AX127153 Sequence

RESULT 1

ALIGNMENTS

AF031478 1859 bp DNA linear PLN 13-JAN-2000
 LOCUS AF031478
 DEFINITION Candida albicans manganese-superoxide dismutase precursor (SOD2)
 gene, complete cds.
 AF031478
 ACCESSION AF031478.1 GI:2623884
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Candida albicans
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 REFERENCE
 1 (bases 1 to 1859)
 Rhee, G.E., Hwang, C.S., Brady, M.J., Kim, S.T., Kim, Y.R., Huh, W.K.,
 Baek, Y.U., Lee, B.H., Lee, J.S., and Kang, S.O. and Kang, S.O.
 Manganese-containing superoxide dismutase and its gene from Candida
 albicans
 JOURNAL Blochim. Biophys. Acta 1426 (3), 409-419 (1999)
 MEDLINE 99177423
 PUBMED 10076057
 2 (bases 1 to 1859)
 Kang, S.O. and Rhee, G.
 Direct Submission
 TITLE Submitted (26-OCT-1997) Microbiology, Seoul National University,
 Shinlim-dong, Kwanak-gu, Seoul 151-742, Republic of Korea
 JOURNAL
 FEATURES
 source
 1. 1859
 /organism="Candida albicans"
 /mol_type="genomic DNA"
 /db_xref="taxon:5476"
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 /protein_id="AA86583.1"
 /db_xref="GI:2623885"
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 ORIGIN
 Alignment Scores:
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 Score: 141.00 Matches: 27
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 Best Local Similarity: 96.43% Mismatches: 1
 Query Match: 97.24% Indels: 0
 DB: 8 Gaps: 0
 US-09-987-190-2 (1-30) x AF031478 (1-1859)
 QY 1 LysTYrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
 Db 950 AAATVTAGTTTACGAAATGACATATGATTCCTCGCTACGACCATCACTTTCTGCT 1009
 QY 21 GlnIleAsnGluIle***TYrThr 28
 Db 1010 CAAATTAACGAATTCACCTACACT 1033
 RESULT 2
 LOCUS CSMNSOD 2332 bp DNA linear PLN 11-MAY-2001
 DEFINITION Candida sp. HN95 MnSOD gene.

ACCESSION Y11598
 VERSION Y11598.1 GI:1877052
 KEYWORDS manganese superoxide dismutase; MnSOD gene.
 SOURCE Candida sp. HN95
 ORGANISM Candida sp. HN95
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; mitosporic Saccharomycetales; Candida.
 REFERENCE
 1
 Hong, Y.M., Nam, Y.S. and Choi, S.Y.
 Molecular Cloning and Characterization of Mn-Superoxide Dismutase
 Gene from Candida sp
 J. Microbiol. 35, 309-314 (1997)
 2 (bases 1 to 2332)
 Choi, S.
 Direct Submission
 TITLE Submitted (04-MAR-1997) S. Choi, HanNam University, Microbiology,
 133 Ojung-Dong, Taeduk-Xu, Taejeon, 300-791, SOUTH KOREA
 JOURNAL
 FEATURES
 source
 1. 2332
 /organism="Candida sp. HN95"
 /mol_type="genomic DNA"
 /strain="HN95"
 /db_xref="taxon:159257"
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 1435. 2332
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 /translation="MLSSAITSASVGIARSRVSVSSGAVRTKVLPLDLMDFGALBP
 HISGQINIEHYTKHQIYVNNINMSIEQAVAKSGEVKLIWALEKALNENG
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 /gene="MnSOD"
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 /product="unnamed"
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 Alignment Scores:
 Pred. No.: 4.35e-09 Length: 2332
 Score: 107.00 Matches: 20
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 Best Local Similarity: 71.43% Mismatches: 4
 Query Match: 73.79% Indels: 0
 DB: 8 Gaps: 0
 US-09-987-190-2 (1-30) x CSMNSOD (1-2332)
 QY 1 LysTYrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20
 Db 1584 AAAGTATGTTTACGAAATGACATTCGAGCTTGGAGCTTGAGACCTCACATTTCCGGA 1643
 QY 21 GlnIleAsnGluIle***TYrThr 28
 Db 1644 CAGATCAACGAATTCACCTACACC 1667
 RESULT 3
 LOCUS AR257498 621 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 23 from patent US 6486382.
 ACCESSION AR257498
 VERSION AR257498.1 GI:27307539
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

```

REFERENCE
  Unclassified.
  1 (bases 1 to 621)
  Gordon-Kamm, W., Pierce, D.A., Bowen, B., Bidney, D., Ross, M.,
  Seeljonge, C., Miller, M.D., Sandahl, G. and Wang, L.
  Use of the green fluorescent protein as a screenable marker for
  plant transformation
  Patent: US 6486382-A 23 26-NOV-2002;
  Location/Qualifiers
    source
      1..621
        /organism="unknown"
        /mol_type="genomic DNA"

ORIGIN
  Alignment Scores:
    pred. No.:      4.52e-09      Length:      621
    Score:          103.00        Matches:      17
    Percent Similarity: 92.86%      Conservative: 9
    Best Local Similarity: 60.71%      Mismatches:  2
    Query Match:    71.03%          Indels:      0
    DB:              Gaps:          0

US-09-987-190-2 (1-30) x AR257498 (1-621)

QY
  1  LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
  ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db
  7  GAGTACACGCTCCCGGATCTGGATTATACGACTACAGCCCTTGGAAACCCACATCTCCGG 66
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QY
  21 GlnIleAsnGluIle**TyrThr 28
  |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db
  67 CAGATCAACGAGCTCGACCATTC 90
  ::::::::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 4
NAU02341
LOCUS
  NAU02341      735 bp      DNA      linear      BCT 12-MAR-1996
DEFINITION
  Nocardia asteroides GUH2 superoxide dismutase gene, complete cds.
ACCESSION
  U02341
VERSION
  U02341.1 GI:484066
KEYWORDS
  .
SOURCE
  .
  Nocardia asteroides
  Nocardia asteroides
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Nocardiaceae; Nocardia.
  1 (bases 1 to 735)
  Alexander, D.J., Chapman, G.D. and Beaman, B.L.
  Isolation, sequencing and expression of the superoxide
  dismutase-encoding gene (sod) of Nocardia asteroides strain GUH-2
  Gene 164 (1), 143-147 (1995)
  96060954
  7590304
  2 (bases 1 to 735)
  Chapman, G.G.
  Direct Submission
  Submitted (01-OCT-1993) Gail D. Chapman, Medical Microbiology and
  Immunology, University of California at Davis, Medical Science
  Building 1A, Davis, CA 95616, USA
  Location/Qualifiers
    1..735
      /organism="Nocardia asteroides"
      /mol_type="genomic DNA"
      /strain="GUH2"
      /db_xref="taxon:1824"
      /clone="clone PAC1500"
      /clone_1b="library EMBL-3"
      99..106
        /note="potential ribosome binding site"
      112..735
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ORIGIN		
Alignment Scores:		
Pred. No.:	5.57e-09	Length: 735
Score:	103.00	Matches: 17
Percent Similarity:	92.86%	Conservative: 9
Best Local Similarity:	60.71%	Mismatches: 2
Query Match:	71.03%	Indels: 0
DB:	1	Gaps: 0
US-09-987-190-2 (1-30) x NAU02341 (1-735)		
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Dd	118 GACTACACCGCTCCGGCATTCGTGATTACGACTACAGCGCCCTGGAACCCCACTCTCCGGG 177	
Qy	21 GnlIleasngIule**TyrThr 28	
Dd	178 CAGATCAACGAGCTGCACCATTC 201	
RESULT 5		
AF333434	657 bp DNA linear BCT 27-AUG-2002	
LOCUS	Mycobacterium avium subsp. paratuberculosis superoxide dismutase	
DEFINITION	gene, complete cds.	
ACCESSION	AF333434	
VERSION	AF333434.2 GI:22507296	
KEYWORDS		
SOURCE		
ORGANISM	Mycobacterium avium subsp. paratuberculosis	
REFERENCE	Mycobacterium avium subsp. paratuberculosis	
AUTHORS	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	
TITLE	Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium	
JOURNAL	avium complex (MAC).	
	1 (bases 1 to 657)	
	Dheenadhayalan,V. and Chang,Y.F.	
	Submitted (04-JUN-2001) Population Medicine and Diagnostic Science,	
	College of Veterinary Medicine, Cornell University, P.O. Box 5786,	
	Ithaca, NY 14853, USA	
	2 (bases 1 to 657)	
	Shin,S.J., Dheenadhayalan,V. and Chang,Y.F.	
	Direct Submission	
	Submitted (27-AUG-2002) Population Medicine and Diagnostic Science,	
	College of Veterinary Medicine, Cornell University, P.O. Box 5786,	
	Ithaca, NY 14853, USA	
REMARK	Sequence update by submitter	
COMMENT	On Aug 27, 2002 this sequence version replaced gi:12247898.	
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	/protein_id="YA650084.2"	
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CDS		
ORIGIN		
Alignment Scores:		
Pred. No.:	1.12e-08	Length: 657
Score:	101.00	Matches: 17

Percent Similarity: 92.86%
 Best Local Similarity: 60.71%
 Query Match: 69.66%
 DB: 1
 Gaps: 0

US-09-987-190-2 (1-30) x AF333434 (1-657)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 DB 40 GAATACACCCCTGCGCCGACCTGAGACTGCGACTATGCACGCTTGAACCGACATCTCGGGG 99
 QY 21 GlnIleAsnGluIle**TyrThr 28
 DB 100 CAGATCAACGAGATCCACACACC 123

RESULT 6
 LOCUS AX708734 900 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 59 from Patent WO02074991.
 ACCESSION AX708734
 VERSION AX708734.1 GI:29564464
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium avium subsp. paratuberculosis
 Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 avium complex (MAC).

REFERENCE
 AUTHORS Karlsen, F.
 TITLE Detection of microorganisms using inducible genes
 JOURNAL Patent: WO 02074991-A 59 26-SEP-2002;
 Norchip A/S (NO)

FEATURES
 source
 1..900
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 FGSPDKPRAQFSAANGIQQSGMAVILGYDTVGSRLTFQLYDQANVPLGITPLLOYD
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ORIGIN

Alignment Scores:
 Pred. No.: 1.66e-08 Length: 900
 Score: 101.00 Matches: 17
 Percent Similarity: 92.86% Conservative: 9
 Best Local Similarity: 60.71% Mismatches: 2
 Query Match: 69.66% Indels: 0
 DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x AX708734 (1-900)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 DB 266 GAATACACCCCTGCGCCGACCTGAGACTGCGACTATGCACGCTTGAACCGACATCTCGGGG 325

QY 21 GlnIleAsnGluIle**TyrThr 28
 DB 326 CAGATCAACGAGATCCACACACC 349

RESULT 7
 LOCUS MAU11550 960 bp DNA linear BCT 25-SEP-1996
 DEFINITION Mycobacterium avium TMC 724 superoxide dismutase (sod) gene,

complete cds.
 ACCESSION U11550
 VERSION U11550.1 GI:555745
 KEYWORDS
 SOURCE
 ORGANISM
 Mycobacterium avium
 Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 avium complex (MAC).

REFERENCE
 AUTHORS Escuyer, V., Haddad, N., Frehel, C. and Berche, P.
 TITLE Molecular characterization of a surface-exposed superoxide
 dismutase of Mycobacterium avium
 JOURNAL Microb. Pathog. 20 (1), 41-55 (1996)
 MEDLINE 96276149
 PUBMED 8692009

REFERENCE
 AUTHORS Escuyer, V.E.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-1994) Vincent E. Escuyer, INSERM
 U411-Microbiologie, Faculte de Medecine Necker, 156 rue de
 Vaugirard, Paris 75015, France

FEATURES
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 /strain="TMC 724"
 /db_xref="taxon:1764"
 /clone="pSOD1"
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 /note="GTG start codon"
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 /transl_table=1
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ORIGIN

Alignment Scores:
 Pred. No.: 1.79e-08 Length: 960
 Score: 101.00 Matches: 17
 Percent Similarity: 92.86% Conservative: 9
 Best Local Similarity: 60.71% Mismatches: 2
 Query Match: 69.66% Indels: 0
 DB: 1 Gaps: 0

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QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 DB 257 GAATACACCCCTGCGCCGACCTGAGACTGCGACTATGCACGCTTGAACCGACATCTCGGGG 316

QY 21 GlnIleAsnGluIle**TyrThr 28
 DB 317 CAGATCAACGAGATCCACACACC 340

RESULT 8
 LOCUS AF180816 1741 bp DNA linear BCT 30-NOV-2001
 DEFINITION Mycobacterium avium subsp. paratuberculosis superoxide dismutase
 (sod) gene, complete cds; and unknown gene.
 ACCESSION AF180816
 VERSION AF180816.1 GI:9957569
 KEYWORDS

SOURCE
ORGANISM
Mycobacterium avium subsp. paratuberculosis
Bacteria: Actinobacteria; Actinobacteriales; Corynebacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
REFERENCE
AUTHORS
1 (bases 1 to 1741)
Liu, X., Feng, Z., Harris, N.B., Cirillo, J.D., Bercovier, H. and Barletta, R.G.
TITLE
Identification of a secreted superoxide dismutase in Mycobacterium avium ssp. paratuberculosis
JOURNAL
FEMS Microbiol. Lett. 202 (2), 233-238 (2001)
MEDLINE
21411748
PUBMED
11520620
REFERENCE
AUTHORS
2 (bases 1 to 1741)
Liu, X., Feng, Z., Cirillo, J. and Barletta, R.G.
TITLE
Direct Submission
JOURNAL
Submitted (25-AUG-1999) Veterinary and Biomedical Sciences, University of Nebraska-Lincoln, Fair Street and East Campus Loop, Lincoln, NE 68583-0905, USA
FEATURES
source
Location/Qualifiers
1. 1741
/organism="Mycobacterium avium subsp. paratuberculosis"
/mol_type="genomic DNA"
/strain="K-10"
/sub_species="paratuberculosis"
/db_xref="taxon:1770"
260..883
/gene="sod"
260..883
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/transl_table=11
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/protein_id="AA09425.1"
/db_xref="GI:9957590"
/translation="MAEYTLPDLDMDYALEPHISGOINIEHTKHAATYKGVNDALAKLEBANADPHAIPLNEKNLAFHGLGHVHSHIMWNLSLSPDGDKRTGELAAIDDAFGSDKRAQPSAANGLOSGMAVLCYDTVGSLLTFOLYDQANVPLGIIPLLQVDMMHAFYLYQKNVADYKAFMNVNVAADVQKRYAATSKAQGLIFG"
1041..1574
/note="similar to Mycobacterium tuberculosis hypothetical protein RV3847"
/codon_start=1
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/product="unknown"
/protein_id="AA09426.1"
/db_xref="GI:9957591"
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ORIGIN
Alignment Scores:
Pred. No.: 3,76e-08 Length: 1741
Score: 101.00 Matches: 17
Percent Similarity: 92.86% Conservative: 9
Best Local Similarity: 60.71% Mismatches: 2
Query Match: 69.66% Indels: 0
DB: 1 Gaps: 0
US-09-987-190-2 (1-30) x AF180816 (1-1741)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
Db 266 GAATACACCTGCTGCCGACCTGGACTGAGCTATGACGCTGTGAACCGCACATCTGGGG 325
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 326 CAGATCAACGATCCACACACACC 349
RESULT 9
D13288

LOCUS
D13288 815 bp DNA linear BCT 17-JUN-1998
DEFINITION
Mycobacterium lepraemurium DNA for Mn superoxide dismutase, complete cds.
ACCESSION
D13288
VERSION
D13288.1 GI:3228263
KEYWORDS
Mn superoxide dismutase.
SOURCE
Mycobacterium lepraemurium
ORGANISM
Mycobacterium lepraemurium
Bacteria: Actinobacteria; Actinobacteriales; Corynebacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
1 (bases 1 to 815)
Nakamura, M.
JOURNAL
Unpublished
REFERENCE
AUTHORS
2 (bases 1 to 815)
Nakamura, M.
TITLE
Direct Submission
JOURNAL
Submitted (21-SEP-1992) Masahiko Nakamura, Osaka University, Institute for Protein Research; 3-2 Yamadaoka, Suita, Osaka 565, Japan (E-mail: masahiko@protein.osaka-u.ac.jp, Tel:06-879-8628, Fax:06-879-8629)
FEATURES
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Location/Qualifiers
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/strain="Hawaiian"
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94..717
/codon_start=1
/transl_table=11
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/protein_id="BA28850.1"
/db_xref="GI:3228264"
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ORIGIN
Alignment Scores:
Pred. No.: 2.23e-08 Length: 815
Score: 100.00 Matches: 17
Percent Similarity: 89.29% Conservative: 8
Best Local Similarity: 60.71% Mismatches: 3
Query Match: 68.97% Indels: 0
DB: 1 Gaps: 0
US-09-987-190-2 (1-30) x D13288 (1-815)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPhseSerAlaThrGluProTyrIleSerGly 20
Db 100 GAATACACCTGCTGCCGACCTGGACTGAGCTATGAAAGCTTGAAACCGCACATCTCGGG 159
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 160 CAGATTACGATCCACACACACC 183
RESULT 10
CNS06105
LOCUS
DEFINITION
T3 end of clone AS0AA022C08 of library AS0AA from strain CLIB 533 of Saccharomyces bayanus, sequence tagged site.
ACCESSION
AL400539
VERSION
AL400539.1 GI:12156708
KEYWORDS
STS.
SOURCE
Saccharomyces bayanus
ORGANISM
Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE
AUTHORS
1 (bases 1 to 908)
Souci, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolestin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,

```

de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Ilorente, B.,
Malpertuy, A., Neuvéglise, C., Ozler-Kalogenopoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Weslowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
Yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
JOURNAL MEDLINE 20584711
PUBMED 11152876
2 (bases 1 to 908)
Bon, E., Neuvéglise, C., Casaregola, S., Artiguenave, F., Wincker, P.,
Aigle, M. and Durrens, P.
Genomic exploration of the hemiascomycetous yeasts: 5.
Saccharomyces bayanus var. uvarum
FEMS Lett. 487 (1), 37-41 (2000)
JOURNAL MEDLINE 20584715
PUBMED 11152880
3 (bases 1 to 908)
Genoscope.
TITLE Direct Submission
AUTHORS Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,
JOURNAL 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
Source
Location/Qualifiers
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/variety="uvarum"
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/clone_11b="AS02A"
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similarity to S.pombe hypothetical protein ]
1 putative frameshift(s)"
/evidence=not_experimental
<673..>906
/note="similar to Saccharomyces cerevisiae ORF YHR008C [
SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial
]"
/evidence=not_experimental
misc_feature
<4..>239
/note="similar to Saccharomyces cerevisiae ORF YHR009C [
similarity to S.pombe hypothetical protein ]
1 putative frameshift(s)"
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SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial
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misc_feature
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/note="similar to Saccharomyces cerevisiae ORF YHR009C [
similarity to S.pombe hypothetical protein ]
1 putative frameshift(s)"
/evidence=not_experimental
<673..>906
/note="similar to Saccharomyces cerevisiae ORF YHR008C [
SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial
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/evidence=not_experimental
ORIGIN
Alignment Scores:
Pred. No.: 2,55e-08 Length: 908
Score: 100.00 Matches: 18
Percent Similarity: 82.14% Conservative: 5
Best Local Similarity: 64.29% Mismatches: 5
Query Match: 68.97% Indels: 0
DB: 11 Gaps: 0
US-09-987-190-2 (1-30) x CNS06105 (1-908)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 751 AAAGTCACCTTCGACAAACCTAAAGTGGAGATTGTGGGCGCTTTGGAAACCTATATTTCGGGC 810
QY 21 GlnIleAsnGlnIle***TyrThr 28
Db 811 CAAATCAACGAATTCATTACACC 834

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RESULT 11
SCSDMNG      2045 bp      DNA      linear      PLN 04-DEC-1994
LOCUS        yeast gene for mitochondrial manganese superoxide dismutase (MnSOD)
DEFINITION   (Chromosome VIII, between centromere and arg4).
ACCESSION    X02156
VERSION      X02156.1
KEYWORDS     GI:4513
SOURCE       Saccharomyces cerevisiae (baker's yeast)
ORGANISM     Saccharomyces cerevisiae
REFERENCE    1. (bases 1 to 2045)
AUTHORS      Sakayota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
              Saccharomycetales; Saccharomycetaceae; Saccharomyces.
              Marres,C.A., Van Loon,A.P., Oudshoorn,P., Van Steeg,H.,
              Grivell,L.A. and Slater,E.C.
              Nucleotide sequence analysis of the nuclear gene coding for
              manganese superoxide dismutase of yeast mitochondria, a gene
              previously assumed to code for the Rieske iron-sulphur protein
              Eur. J. Biochem. 147 (1), 153-161 (1985)
TITLE        Data kindly reviewed (07-JUL-1986) by A.P.G.M. Van Loon.
JOURNAL      Location/Qualifiers
MEDLINE      1. .2045
PUBMED       /organism="Saccharomyces cerevisiae"
COMMENT       /mol_type="genomic DNA"
FEATURES      /strain="PL 100"
              /db_xref="taxon:4932"
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              /db_xref="GI:600040"
              /db_xref="SPTREMBL:Q07073"
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              LFLFLSWRLSYLP.LRMVRLHV"
              218..239
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              reg. of MnSOD expression"
              311..329
              /note="put. UAS2"
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              /db_xref="SGD:S0001050"
              /db_xref="SMISS-PROT:P00447"
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              GFTHCELFWENLAPESQSGSPPGALAKAIDEPGSLDELIKLTKLKGVSQNA
              FIVNLNSGGLDVQTVQNDTVGPLVPAIDAWEHAYVLQYONRKADYFKAIMNV
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              /note="unnamed protein product; URF 2"
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              /db_xref="GI:4517"
              /db_xref="SPTREMBL:Q07074"
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              TRTHHQENQLFLILFPQIVKPLRS"
ORIGIN
Alignment Scores: 6.97e-08 Length: 2045

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Score:	Percent Similarity:	Matches:
Best Local Similarity:	82.14%	Conservative:
Query Match:	64.29%	Mismatches:
	68.97%	Indels:
		Gaps:

US-09-987-190-2 (1-30) x SCSODMNG (1-2045)

QY 1 LyeTyrSerIeuProGluIeuAspTYrGluPheSerAlaThrGluProTYrIleSerGly 20

Db 637 AAGTACACCTTGGCAGACTTGAAGTGGAGACTTGGTGCACACTGGAACCTTATCTCCGCT 696

QY 21 GHIILASNGIuile**TYrThr 28

Db 697 CAAATCAACGAATTGCATTACACC 720

RESULT 12
YSCHE2825/c

LOCUS YSCHE2825 18715 bp DNA linear PLN 04-SEP-1997

DEFINITION Saccharomyces cerevisiae chromosome VIII cosmid I2825.

ACCESSION U10400 U00093

VERSION U10400.1 GI:500701

KEYWORDS

SOURCE

ORGANISM

Saccharomyces cerevisiae (baker's yeast)

Saccharomyces cerevisiae

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 18715)

Johnston,M., Andrews,S., Brinkman,R., Cooper,J., Ding,H., Dover,J., Kucaba,T., Hillier,L., Jier,M., Johnston,L., Keppler,D., Langston,Y., Latreille,P., Louis,E., Macri,C., Mardis,E., Mousier,L., Nhan,M., Rifken,L., Riles,L., St.Peter,H., Thornton,L., Trevisan,E., Vaudin,M., Vaughan,K., Vignati,D., Wilcox,L., Willis,A., Wilson,R., Wohlman,P. and Waterston,R.

Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII

Science 265 (5181), 2077-2082 (1994)

JOURNAL MEDLINE 94378003

PUBMED 8091229

REFERENCE 2 (bases 1 to 18715)

AUTHORS Du,Z.

TITLE The sequence of S. cerevisiae cosmid I2825

JOURNAL Unpublished (1994)

REFERENCE 3 (bases 1 to 18715)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-1994)

REFERENCE 4 (bases 1 to 18715)

AUTHORS Jia,Y. and Cherry,J.M.

TITLE Direct Submission

JOURNAL Submitted (04-SEP-1997)

COMMENT Department of Genetics, Stanford University, Saccharomyces Genome Database, Stanford, CA 94305-5120, USA

COMMENT Curated by:
Saccharomyces Genome Database
URL: <http://genome-www.stanford.edu/>
e-mail: yeast-curator@genome.stanford.edu

Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: mj@sequencer.wustl.edu

NEIGHBORING COSMID INFORMATION:

This sequence includes nucleotides 1-17118 of lambda clone YSCHE2825. It overlaps with the cosmid on the left (YSCHE9780) by 800 bp; with the cosmid on the right (YSCHE8082) by 1001 bp.

Location/Qualifiers

source

1. .18715
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/db_xref="taxon:4932"
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complement (128. .829)
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complement (128. .829)
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/note="YHR008c"
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/protein_id="AAB68939.1"
/db_xref="GI:500704"
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GFNFHQLFENLALPSOGGGEPTGALKALIDQFGLDELILKLTNKLAVGSSGNA
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VMKXSRREFDAGKI"
complement (1348. .2904)
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complement (1348. .2904)
/gene="YHR009c"
/codon_start=1
/evidence=not experimental
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/protein_id="AAB68938.1"
/db_xref="GI:500703"
/translacion="MAHPPTQYPSKNSBKKKHIVVGGIIGCCTAYTLTHPSFSPS
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SLKNSASNEEGESDIIHVSSPSLHSLITNRRMSHNSASDIDSVSPVQILBETHN
NPLADLMIRRELINMDSSLSGGDTTRQQLHPYKFTFPIISKAFETGAVDLLGKVG
LKCDMDCHSKLTIPLSVYKNNRNSRGAENPDIKLGTINDENAKFIEINDIQQVL
SNKPTSTSLKDCPLSGLRASHVTIKSEKTVSPYALALAKVNDREFSPENYARD
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/db_xref="GI:500709"
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QYNQNSKSEELKIKLETCKSLPTLIDPVLDAPOIOWINPLKTHTSFOAHVD
IMLKNMLDLQTSANVTGMSWYLLNDGARLBQALVAVALKANENGSSCYPSBITK
KELIDAGSPRRMNERQIYALQTNIGLVATAEIPLAGLANKVLENSGSCKL
VGVRCTRAAGARGKDTKGLTVRHEFTYELPCKMSKPTSAKVIIEIKQFIIVEE
LGIPAKLVNPSDLQGNPAKRYDIEAMVGRGKFEISASNCYDFQSRRLNTYYR
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 /evidence=not_experimental
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 /db_xref="GI:500712"
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 DMPVTFVDSQDEAVTSVDKPKENQSEDDAKGSGTGEQGSITPKEGTAGESEN
 ENENSVKRENFQKFEVDMSDSDINGNSPFLDLIQGNTCTLYLYLVNGEVKVDK
 VYVERE"
 complement(7968. .8684)
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 complement(7968. .8684)
 /gene="YHR013C"
 /note="YHR013C"
 /codon_start=1
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 /db_xref="GI:500702"
 /translation="MPINIRATINDIICQANLHNLPENYMKTYMYHILSWPEAS
 FVATTTLDGSDSDENDKDLFLDGTNGDRTIKDPPYLAAGEKLVGYLVAKND
 DPDOONEPNNHTISLSTMYRTRMGIAENIMRQALPALREYQAEVSLIHWQSRRA
 ALHTRPDLAEVTSISKSYQDGEDAVAKKYLKLELQISNFTIRRLKENEKLED
 DLESDLEDITIKQVNDIIV"
 9284. .10159
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 /db_xref="GI:500706"
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 PSPMNVFSQYQVGNPFTFLPSHPNINVAIPQRELLYENVAIVDSPLFKKTRLP
 HQTSLIDKRNKQYDLPIYVSIINNGDFVQETPRAPKSKRLSTLNDVNCSDYES
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 /product="tRNA-Ser"
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 11559. .11630
 /gene="tQ(UUG)H"
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 /note="codon recognized: CAA"
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 N-terminus."
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 /db_xref="GI:500707"
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Alignment Scores:

Pred. No.:	1.09e-06	Length:	18715
Score:	100.00	Matches:	18
Percent Similarity:	82.14%	Conservative:	5
Best Local Similarity:	64.29%	Mismatches:	5
Query Match:	68.97%	Indels:	0
DB:	8	Gaps:	0

US-09-987-190-2 (1-30) X YSCHL2825 (1-18715)

DQ 751 AAGTCACCTTGGCCGACTTGAAAGTGGACTTCGGGCATTGGGAACCTTTATATCTCCGCT 692

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QY      21  GlnIleasnGluIle**TyrThr 28
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Db      691  CAAATCAACGAATTCATTACACC 668

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RESULT 13			
YSCH9780/c			
LOCUS	YSCH9780	24431 bp	DNA linear PLN 03-SEP-1997
DEFINITION	Saccharomyces cerevisiae chromosome VIII cosmid 9780.		

VERSION	U10555.1	GI:500813
KEYWORDS		
SOURCE	Saccharomyces cerevisiae (baker's yeast)	
ORGANISM	Saccharomyces cerevisiae	

REFERENCE
AUTHORS
1 (bases 1 to 2431)
Johnston, M., Andrews, S., Brinkman, R., Cooper, J., Ding, H., Doyer, J., G...

TITLE	Author
Complete nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome VIII	Prokhorova, L. I., Naumova, V. A., Tretyakova, E., Vaidina, M., Vaughan, K., Vignati, D., Wilcox, L., Willis, A., Wilson, R., Wohldman, P. and Waterston, R.

JOURNAL Science 265 (5181), 2077-2082 (1994)
MEDLINE 94378003

REFERENCE	
AUTHORS	
TITLE	
2	(bases 1 to 24431)
	Favella, T.
	The sequence of S. cerevisiae cosmid 9780

JOURNAL Unpublished (1994)
REFERENCE 3 (bases 1 to 24431)

AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUN-1994)

REFERENCE	4 (bases 1 to 24431)
AUTHORS	Jia, Y. and Cherry, J.M.
TITLE	Direct Submission
JOURNAL	Submitted (03-SEP-1997)

COMMENT

Curated by:
Saccharomyces Genome Database
URL: <http://genome-www.stanford.edu/>
e-mail: yeast-curator@genome.stanford.edu

Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA
e-mail: mj@sequencer.wustl.edu

NEIGHBORING COSMID INFORMATION:

This sequence includes nucleotides 10590-34824 of cosmid 9780. The adjacent clone on the right is YSCH2825. The adjacent clone on

the left is YSCHL5018.

FEATURES
source
Location/Qualifiers
1..24431
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/mol_type="genomic DNA"
/strain="S288c (AB972)"
/db_xref="taxon:4932"
/map="VII1"
90..1274
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/note="MRP4"
90..1274
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/note="MRP4"
/codon_start=1
/product="Mrp4: Mitochondrial ribosomal protein"
/protein_id="AAB6428.1"
/db_xref="GI:500819"
/translation="MQRHVAFNRRRLSLRNPSTKRFQSSASGAANTPNNDEWTL
LOQKLYADEIRSELKSLQVPEDELPELKSLBEDKLSDEQQLAEALSDFFERNYAL
LNKLFDKSLTNGQSSSTTTAAATPKPYNNLIPSAADKPYSSQELFRLQINSMRYAKL
GATISKVYPRKDIYPLPENITVESLMSAGVHIGQSTLSMRSSQSYIGEYGGIH
IIDLQTLSTYKRAKAVGVESGGIILFLGTRQGRGLEAAKTHGYVSTRMI
PGTLNSTEISGIWEKCEIDSDNPTERALSNETSKQVKPDILVIVNPTENRNALLE
AKSRVPRIALIDTSEPSIVTYPIDNDDLSRVNPLGLVLAARGGGLQRRLARRN
EK"
complement(1519..2754)
/gene="LAG1"
complement(1519..2754)
/gene="LAG1"
/note="YHL003C: Similar to UOG1, hypothetical protein in
GDF-1.5' region (mouse and human). Null mutant shows
reduced mean and maximum life span"
/codon_start=1
/evidence=not experimental
/product="lag1p"
/protein_id="AAB6429.1"
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ASKNEAKKRMALTGDSKSDILMKVWFSYRENNYHSMTPFLLVCYSAFLSG
NRTESNPLHMFVAISYVDGDSYAKGIDLSFVFNIFPTFLREFLMVDVIRPFVY
YLNATSEHROKRMLOMAYIYCGVSGPGIYIMHSDIMLFTKPMVRYRYPVTNPF
LFIKIFYGOAFAFMAQACVILQLEKPRKDKELVPHHIVYLLINSSYFHTKGL
ALYITMDVSDPELSLSTKTYLNSVFTFPFGFLVFWIYDRHVNIRIIMSVTEER
HEGVYVNFATQYQKWCISLPIFVLIAALQVNLVYMLFILRLYLWIOGIDKDR
SDSDSESAENESKEKCE"
3482..4840
/gene="YHL002w"
3482..4840
/gene="YHL002w"
/note="Similar to several proteins with SH3 domains"
/codon_start=1
/evidence=not experimental
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/db_xref="GI:500818"
/translation="MSSSAIKRNALIKATDPKIRSDNNQYIILDVCDLYEDEDNQ
EWSLIERLEQDQANVILRTLSLTVSLANCSRLQELSSKFTSLYALLIESHY
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NSDDELQKALKMSLFEYKOKLQOEKESAVLPQOOOHOONQAPAKHAKIACQV
VRVRAIYDLTNEDELSPFKGVITVLEQVYRDMKALRGMGKIPNVTYPIVE
PSKEIEKENKEAIVFSOKTTIDOLHNSNAAKSGNSNEVQDPIGDMTSVTL
RQVTRMLGKYAKEKEDMSLROYLANAESYVQMDRANAHISPPVSPALVAGNT
HANNTVMPQROSYOSNEYSPPSNLPIDHPTNSANNTPOYGYDGLYSVSPPGY
EQ"
5147..5961
/gene="RPL14B"
join(5147..5275,5674..5961)
/gene="RPL14B"
/note="YHL001W; identical to hypothetical protein YKL006w
on chromosome 11"
/codon_start=1
/evidence=not experimental
/product="Rpl14bp: Probable 60S ribosomal protein L44B"
/protein_id="AAB6426.1"

misc_feature
complement(6456..6480)
/note="misc feature comment"
complement(6481..6565)
/note="misc feature comment"
complement(6566..6573)
/note="misc feature comment"
6925..8238
/gene="YHR01w"
6925..8238
/gene="YHR01w"
/note="weakly similar to 60 kD chaperonin (Rickettsia
tsutsugamushi)"
/codon_start=1
/evidence=not experimental
/product="Yhr01w"
/protein_id="AAB6425.1"
/db_xref="GI:500816"
/translation="MALNKLNNIDSLNSSHSSINGIASNANSPSGADTDDIDEND
ESGGSILNIIISQKPGCDLSRITLPTPLIEKKSMLERITVLOLPDVLIAHNSKDG
LQRFVAVAWYLAGMHIGRAVKKRPLNILEHPTAYWDLPNKQAFYIARQTSHP
ESAYFMIPESENIRVDGVVPRKSLGSSANAMEGLVLOFLIDKANGDEKXTLS
QPNVYAGILRFKMRILELGDHVMIMGVQVQDIEPKTGFTSGTYDAIEGTHKIDYK
EYQISGMNDIMYIKDLREKSSKKTUFDHQHPLAKVPLVEQGEYSRIMWK
VTDLAVRDEHVAIEERQLENRQRELAKRAEDGVEFHSKLFRRABEGEDLDVYIYK
HIPGCTKHQEEQINSILETAPILPGQTFTEKFSIPAYKKGIQKN"
8966..8992
/gene="QCR10"
join(8696..8701,8756..8992)
/gene="QCR10"
/note="YHR01W-A"
/codon_start=1
/product="Qcr10p: 8.5 kDa subunit of the guinol cytochrome
oxidoreductase complex"
/protein_id="AAB6434.1"
/db_xref="GI:2351226"
/translation="MALIQYSLSSKTLGHLFGLSLRSRLTAVANIMLWGASMLGL
FVLEPGMKQDDLYKKIPILGPTLEDHTPEDKPN"
9682..10755
/gene="YHR002w"
9682..10755
/gene="YHR002w"
/note="Belongs to the mitochondrial ADP,ATP carrier
protein family"
/codon_start=1
/evidence=not experimental
/product="Yhr002w"
/protein_id="AAB6424.1"
/db_xref="GI:500815"
/translation="MTRDSPSDNSYKINKNTQKTSFDRNSFDYIVRSLAGAGISG
SCAKTLIAPLDRIKILFQTSNPHYTKYTGSLIGLVEAKHIMINDGVRFGQSGSATL
LRIPYAAVYVBOIENRNLIPSKESHSVLAAGSLAGTSVETTPLDIYRVL
AYTEHKRVYLGRIIKKIYKEPASAATLIRKNDYIPNMCCHNCNTRGVYIVLGTPLA
GVSFPHDLHDHDKLFFRPVSVLEISDEBERVQKRRRLPRTVAELISGLLPA
ASQTAIVPELIRRLQVSAISPKTYDHRFQSISETAHIIIFKRGVGRFVGLISGY
IKVTPVACSFYERKWNFGI"
complement(10898..12187)
/gene="YHR003C"
complement(10898..12187)
/gene="YHR003C"
/note="Weak similarity to thif (E. coli), moeb (E. coli),
and ubiquitin activating enzyme (wheat)"
/codon_start=1
/evidence=not experimental
/product="Yhr003cp"
/protein_id="AAB6430.1"
/db_xref="GI:500821"
/translation="MANNTWKLIATATLALISVESTOLAKSVMKREKLSAANKKTVSR
PRQYDHLFRQELARNYAFLEGEMKRIEYIVIVAGAEVGSWCTMLIRSGCCKIM
IIDPENISIDSINTHCCAVLSDIGKPKVQCIKHLHSKIPWSEIKARAKAWIKENSHD

LIPADGSPFTIYDCJDNLESKYDLLEVAHHNKIDVISSMGVATKSDPTRVSLINDISM

Alignment Scores:

Pred. No.: 1,51e-06 Length: 24431
 Score: 100.00 Matches: 18
 Percent Similarity: 82.14% Conservative: 5
 Best Local Similarity: 64.29% Mismatches: 5
 Query Match: 68.97% Indels: 0
 DB: 8 Gaps: 0

US-09-987-190-2 (1-30) x YSC9780 (1-24431)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 24382 AAATGACCTTGCCGACCTGAGACTGGGACTTCGCTGATTGGAACCTTATATCTCCGGT 24323

Qy 21 GlnIleAsnGluIle***TyrThr 28

Db 24322 CAATCAACGATTCGATTACACC 24299

RESULT 14

AF061031

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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REFERENCE

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/organism="Mycobacterium fortuitum"
/mol_type="genomic DNA"
/strain="ATCC 6841"
/db_xref="taxon:1766"
/clone="PMFV1"
/clone_1ib="E.coli TGI"
243..250
257..880
/gene="Sod"
257..880
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/transl_table=11
/product="superoxide dismutase"
/protein_id="CA50266.1"
/db_xref="GI:950079"
/db_xref="GOA:Q59519"
/db_xref="SWISS-PROT:Q59519"
/translation="MAEYTLPLDLDYDGALEPHISGQINELHSHKHAAYKGVNDAY
FGSPDKFQAQPTAAANGIQSGMAVLGSDTLTFLQLDQGANVPLGIIPLLQVD
WHEAFYIQYKNVADYVKAFWNVNMDVONRYAATSKTNGLIFG"

ORIGIN
Alignment Scores:
Pred. No.: 7.09e-08 Length: 1478
Score: 99.00 Matches: 16
Percent Similarity: 89.29% Conservative: 9
Best Local Similarity: 57.14% Mismatches: 3
Query Match: 68.28% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x MFSODA (1-1478)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 GAATACACTTGGCGACCTGCGATTACGACTACGAGACGACGAGCCCACTCTCGGG 322

QY 21 GlnIleSngIle***TyrThr 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 323 CAGATCAACGAGCTCCACACAGC 346

RESULT 16
MLEPSSOD
LOCUS
DEFINITION
Mycobacterium leprae DNA for manganese superoxide dismutase (EC
1.15.1.1).
X16453
X16453.1 GI:44405
manganese superoxide dismutase; metalloenzyme; superoxide
dismutase.
SOURCE
Mycobacterium leprae
ORGANISM
Mycobacterium leprae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 649)
Thangaraj,H.S., Lamb,F.I., Davis,E.O. and Colston,M.J.
Nucleotide and deduced amino acid sequence of Mycobacterium leprae
manganese superoxide dismutase
Nucleic Acids Res. 17 (20), 8378 (1989)
JOURNAL
MEDLINE
90045970
PUBMED
2682526
2 (bases 1 to 649)
Thangaraj,H.S.
DIRECT SUBMISSION
Submitted (01-SEP-1989) Thangaraj H.S., National Institute for
Medical Research, Laboratory of Leprosy and Mycobacterial Research,
Mill Hill, London NW7 1AA, UK
FEATURES
source
1..649
Location/Qualifiers
/organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db_xref="taxon:1769"

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/clone="Y3164 and pHT7"
/clone_1ib="lambda gcl1 and pHC79 cosmid"
1..4
/note="pot. ribosome binding site"
14..637
/note="unnamed protein product; superoxide dismutase (AA
1-207)"
/codon_start=1
/transl_table=11
/protein_id="CA34472.1"
/db_xref="GI:581343"
/db_xref="GOA:P13367"
/db_xref="SWISS-PROT:P13367"
/translation="MAEYTLPLDLDYDGALEPHISGRINEITHTHKHAAYKGVNDAL
AKLEAPAKDHSALFLNEKULAPHLGCVHNSIMWKULSPGSGDKPTGGLATIDET
FGSPDKFQAQPTAAANGIQSGMAVLGSDTLTFLQLDQGANVPLGIIPLLQVD
WHEAFYIQYKNVADYVKAFWNVNMDVONRYAATSKTNGLIFD"

ORIGIN
Alignment Scores:
Pred. No.: 3.89e-08 Length: 649
Score: 98.00 Matches: 16
Percent Similarity: 92.86% Conservative: 10
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 67.59% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x MLEPSSOD (1-649)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 GAATACACCTTGGCGACCTTGGACTGGGACTACGAGGCGCTGACACACATCTCTGCT 79

QY 21 GlnIleSngIle***TyrThr 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 GAGATCAACGAGATCCACACACC 103

RESULT 17
MLEPRTN/c
LOCUS
DEFINITION
Mycobacterium leprae strain TN complete genome; segment 1/10.
AL583917 AL450380
X1583917.1 GI:13092412
VERSION
KEYWORDS
SOURCE
Mycobacterium leprae
ORGANISM
Mycobacterium leprae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 344050)
Cole,S.T., Bigmeier,K., Parkhill,J., James,K.D., Thomson,N.R.,
Wheeler,P.R., Honore,N., Ganter,T., Churcher,C., Harris,D.,
Mungall,K., Basham,D., Brown,D., Chillingworth,T., Connor,R.,
Davies,R.M., Devlin,K., Dutfoy,S., Feltwell,T., Fraser,A.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Lacroix,C.,
Maclean,J., Moule,S., Murphy,L., Oliver,Quail,M.A.,
Rajandream,M.-A., Rutherford,K.M., Rutter,S., Seeger,K., Simon,S.,
Simmonds,M., Skelton,J., Squares,R., Squares,S., Stevens,K.,
Taylor,K., Whitehead,S., Woodward,J.R. and Barrell,B.G.
Massive gene decay in the leprosy bacillus
Nature 409 (6823), 1007-1011 (2001)
JOURNAL
MEDLINE
21128732
PUBMED
11234002
2 (bases 1 to 344050)
Parkhill,J.
DIRECT SUBMISSION
Submitted (20-FEB-2001) Submitted on behalf of the Mycobacterium
leprae sequencing teams, The Sanger Centre, Wellcome Trust Genome
Campus, Hinxton, Cambridge, CB10 1SA, UK Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724, Paris Cedex, France. E-mail: parkhill@sanger.ac.uk
Notes:
Details of M. leprae sequencing at the Sanger Centre are available
from http://www.sanger.ac.uk/Projects/M_leprae/ A relational

```

COMMENT

database containing the M. leprae sequences is available from
http://genolist.pasteur.fr/Leprae/.

Location/Qualifiers

FEATURES

source

1. .344050

/organism="Mycobacterium leprae"

/mol_type="genomic DNA"

/strain="TN"

/db_xref="taxon:1769"

1. .1566

/gene="dnaA"

/note="synonym: ML0001"

1. .1566

/gene="dnaA"

/note="Similar to M. tuberculosis dnaA, chromosomal

replication initiator protein, SW:DNA_MYCTU (P49993) (507

aa); Fasta score E(): 0, 87.2% identity in 507 aa overlap

and Mycobacterium smegmatis dnaA, SW:DNA_MYCSM (P49992)

(495 aa); Fasta score E(): 0, 69.2% identity in 441 aa

overlap. Previously sequenced as SW:DNA_MYCLE (P46388)

(521 aa); Fasta score E(): 0, 99.8% identity in 521 aa

overlap. Contains Pfam match to entry PF00308 bac_dnaA,

Bacterial dnaA protein. Contains PS00017 ATP/GTP-binding

site motif A (P-loop). Contains PS01008 dnaA protein

signature."

/codon_start=1

/transl_table=1

/product="putative chromosomal replication initiator

protein"

/protein_id="CAC29509.1"

/db_xref="GI:13092413"

/db_xref="GOA:P46388"

/db_xref="SWISS-PROT:P46388"

/translation="MEVPHAKPEITYNQORDTSADLSIGFTTWMNAVSENGESN

TDEANIDSLVPLPQORAMNLVPLITIEGFAIJSVSSFVONEIEHLKPLT

DALSRLGQIQGLGVRIAPSTDIIDNSSADVLINDGCTIDENYGEPLTGEYOG

LPVTEPRPHHTSTVIGTSLNRYTEFEVIGASNRFAAALAIAEAPARANPL

PIWESGIGKTHILHAAGNVAORLPQGRVYKVTSEETDINFSLRDPRVAKRSY

RDVVLIVDDIQFIEGKEGIOEFPHNTLNANKQIVISSDRPPKQALTEELRT

RFEGMLITDVPPELETRIALRKKAQERLAVGDVIELASIEENREILBEALIR

VTAFASINKTAIDKALAEIVRLIDASTVQISATITMTATYFPTTIEELGPCK

TRALASROIMVLCRELTDLSPKIQGFGRDHTTWYAKRKILSEMAERREVFHY

KELTFRJROSKR"

544. .1482

/gene="dnaA"

/note="Pfam match to entry PF00308 bac_dnaA, Bacterial

dnaA protein, score 712.20, E-value 8.3e-240"

664. .687

/gene="dnaA"

/note="PS00017 ATP/GTP-binding site motif A (P-loop)"

1426. .1482

/gene="dnaA"

/note="PS01008 DnaA protein signature"

2081. .3280

/gene="dnaA"

/note="synonym: ML0002"

2081. .3280

/gene="dnaA"

/EC_number="2.7.7.7"

/note="Similar to M. tuberculosis dnaA, DNA polymerase

III, [beta] subunit, SW:DP3B_MYCTU (Q50790) (402 aa);

Fasta score E(): 0, 80.9% identity in 403 aa overlap and

Mycobacterium smegmatis dnaA, SW:DP3B_MYCSM (P52851) (397

aa); Fasta score E(): 0, 77.3% identity in 397 aa overlap.

Previously sequenced as SW:DP3B_MYCLE (P46387) (399 aa);

Fasta score E(): 0, 100.0% identity in 399 aa overlap.

Contains Pfam match to entry PF00712 DNA_pol3_beta, DNA

polymerase III beta subunit."

/codon_start=1

/transl_table=1

/product="putative DNA polymerase III, [beta] subunit"

/protein_id="CAC29510.1"

/db_xref="GI:13092414"

/db_xref="GOA:P46387"

misc_feature

2117. .3214

/gene="dnaA"

/note="Pfam match to entry PF00712 DNA_pol3_beta, DNA

polymerase III beta subunit, score 592.70, E-value

2.2e-174"

3281. .4438

/gene="recF"

/note="synonym: ML0003"

3281. .4438

/gene="recF"

/note="Similar to M. tuberculosis recF, DNA replication

and SOS induction protein, SW:RECF_MYCTU (Q59586) (385

aa); Fasta score E(): 0, 76.4% identity in 385 aa overlap

and Mycobacterium smegmatis recF, SW:RECF_MYCSM (P50916)

(384 aa); Fasta score E(): 0, 70.0% identity in 383 aa

overlap. Previously sequenced as SW:RECF_MYCLE (P46391)

(385 aa); Fasta score E(): 0, 99.5% identity in 385 aa

overlap. Contains 2 Pfam matches to entry PF00470 RecF,

RecF protein. Contains PS00617 RecF protein signature 1.

Contains PS00017 ATP/GTP-binding site motif A (P-loop).

Contains PS00618 RecF protein signature 2."

/codon_start=1

/transl_table=1

/product="putative DNA replication and SOS induction

protein"

/protein_id="CAC29511.1"

/db_xref="GI:13092415"

/db_xref="GOA:P46391"

/db_xref="SWISS-PROT:P46391"

/translation="MYVHFGLDFRSMVDVLEINRGTVFPGPNNGKTNLIEALM

YSTLSSRGRTDIPILRAGTIRATVITVYNERECADILEIAGANRANRLRSIV

RGNREYGVRAVLPAPEDIALVCGDANRANRIVADYAPVIAVADYVLRQ

RTALRLKSLAARHSDDGVLPDTPWTRIAEHGAIRMARIDVNLQALPVEVAYQ

LAPGSRVASISYRASIDIGIAGVSSDRALQDLIAGLSTRNVELERICIVGPH

RDELLEIRLGDQPAKGFASHGSMIAIALRLAAVELLRADNEFVLLIDVFAELDA

RCRLATVAESAQEVLTSAQEDIPVGMQAKWTVLDLRDSGSRVSVYP"

3287. .3415

/gene="recF"

/note="Pfam match to entry PF00470 RecF, RecF protein,

score 18.90, E-value 0.00024"

3368. .3391

/gene="recF"

/note="PS00017 ATP/GTP-binding site motif A (P-loop)"

3614. .3691

/gene="recF"

/note="PS00617 RecF protein signature 1"

4100. .4423

/gene="recF"

/note="Pfam match to entry PF00470 RecF, RecF protein,

score 5.20, E-value 1.5"

4244. .4297

/gene="recF"

/note="PS00618 RecF protein signature 2"

4435. .5004

/gene="ML0004"

/note="ML0004"

/note="Similar to hypothetical proteins from mycobacteria

e.g. M. tuberculosis RV0004, hypothetical protein,

TR:P71573 (EMBL:AL124456) (187 aa); Fasta score E(): 0,

77.2% identity in 167 aa overlap. Previously sequenced as

TR:Q50181 (EMBL:Z70722) (199 aa); Fasta score E(): 0,

99.5% identity in 187 aa overlap."

/codon_start=1


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/transl_table=11
/product="conserved hypothetical protein"
/protein_id="CAC29512.1"
/db_xref="GI:13092416"
/db_xref="SWISS-PROT:Q9CDF4"
/translation="MIESNYSYSGDTRTEPGLTSGFDLVRRLAEARAAACAGGK
ACRGHVVPVPRVTDNRNRNMGPGDPDPPDLAKKRGKSAQVAGVFG
QKASWVGQIADHAFPGVNNVSLVTAETMAVQLRMQQLAKIAAAGNGVVT
SIKITPTAPSRKRPWHIAGRPDTYG"
RBS
5211..5216
/feature="possible RBS"
gene
5229..7265
/feature="gyrB"
/feature="synonym: ML0005"
CDS
5229..7265
/feature="gyrB"
/EC_number="5.99.1.3"
/feature="Similar to M. tuberculosis gyrB, DNA gyrase subunit
B, SW:GYRB MYCTU (P41514) (686 aa); Fasta score E(): 0,
87.5% identity in 679 aa overlap and to Mycobacterium

```

Alignment Scores:

```

Pred. No.: 9.3e-05 Length: 344050
Score: 98.00 Matches: 16
Percent Similarity: 92.86% Conservative: 10
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 67.59% Indels: 0
DB: 1 Gaps: 0

```

US-09-987-190-2 (1-30) x MLEPRTN1 (1-344050)

Qy 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 93264 GAATACACCCCTGCCGATTGAGCTGACGACTACGAGCGCTGGAACCATATCTCGGT 93205

Qy 21 GlnIleAsnGluIle***TyrThr 28

Db 93204 GAGATCAACGAGATCCACACACC 93181

RESULT 18

MTSOD

LOCUS MTSOD 790 bp DNA linear BCT 03-MAY-1995
 DEFINITION M. tuberculosis SOD gene.
 ACCESSION X52861
 VERSION X52861.1 GI:794079
 KEYWORDS sod gene; superoxide dismutase.
 SOURCE Mycobacterium tuberculosis
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 1 (bases 1 to 790)
 Zhang, Y., Lathigra, R., Garbe, T., Gatty, D. and Young, D.
 Genetic analysis of superoxide dismutase, the 23 kilodalton antigen
 of Mycobacterium tuberculosis
 JOURNAL M.O. Microbiol. 5 (2), 381-391 (1991)
 MEDLINE 91251768
 PUBMED 1904126
 2 (bases 1 to 790)
 Zhang, Y.
 Direct Submission
 Submitted (23-APR-1990) Zhang Y., MRC TB & Related Infections Unit,
 Cyclotron Bldg, Hammersmith Hospital, London W12 0HS, U K
 On May 4, 1995 this sequence version replaced gi:44678.
 Data kindly reviewed (02-JUL-1990) by Zhang Y.
 Related sequence: S36714.
 Location/Qualifiers
 1..790
 /organism="Mycobacterium tuberculosis"
 /mol_type="genomic DNA"
 /strain="H37Rv"
 /db_xref="taxon:1773"
 /clone="YA3P-9"

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source

```

-35_signal
20..25
/feature="putative"
RBS
99..105
gene
112..735
/feature="SOD"
112..735
/feature="SOD"
CDS
112..735
/feature="SOD"
/EC_number="1.15.1.1"
/codon_start=1
/translation_except=(pos:112..114,aa:Met)
/transl_table=11
/product="superoxide dismutase"
/protein_id="CAA37042.1"
/db_xref="GI:581379"
/db_xref="GOA:P17670"
/db_xref="SWISS-PROT:P17670"
/translation="MAEYTLPLDMDYGALEPHISQINELHSHKHATYYKANDAV
AKLEEARAKEDHSAIILNENKILARLHAGVHTIIMWKLI.SPGGDKPTEGELAAATADA
FGSPDKFPAQPHAAATTVQSGMAALGMDITLGNKLLIFQYVDHOTNPGLIVPLILLD
MMEHAFYLIQYKNVAVDFAKAFNNVNMADVDSRYAAATISQTKGLIFG"

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ALIGNMENT Scores:

```

Pred. No.: 2.66e-07 Length: 790
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 1 Gaps: 0

```

US-09-987-190-2 (1-30) x MTSOD (1-790)

Qy 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 118 GAATACACCTTGCCAGACTGAGCTGAGACTACGAGACTGGAACCATATCTCGGT 177

Qy 21 GlnIleAsnGluIle***TyrThr 28

Db 178 GAGATCAACGAGCTTCACACACC 201

RESULT 19

AF077406

LOCUS AF077406 943 bp DNA linear BCT 26-JUL-1998

DEFINITION Mycobacterium bovis BCG superoxide dismutase (SOD) gene, complete

ACCESSION AF077406 GI:3342171

VERSION AF077406.1

KEYWORDS

SOURCE

ORGANISM

Mycobacterium bovis BCG
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 1 (bases 1 to 943)
 Kimble, E., Sanderson, R.J. and Gill, R.E.
 Superoxide dismutase of M. bovis BCG
 JOURNAL Unpublished
 2 (bases 1 to 943)
 Kimble, E., Sanderson, R.J. and Gill, R.E.
 Direct Submission
 Submitted (10-JUL-1998) Microbiology, University of Colorado Health
 Sciences Center, 4200 E. 9th Ave., Denver, CO 80220-3706, USA
 Location/Qualifiers
 1..943
 /organism="Mycobacterium bovis BCG"
 /mol_type="genomic DNA"
 /strain="Pasteur"
 /db_xref="taxon:33892"
 /db_xref="GOA:P17670"
 /feature="SOD"
 307..314
 /feature="SOD"

FEATURES

source

1..943
 /organism="Mycobacterium bovis BCG"
 /mol_type="genomic DNA"
 /strain="Pasteur"
 /db_xref="taxon:33892"
 /db_xref="GOA:P17670"
 /feature="SOD"
 307..314
 /feature="SOD"

CDS

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/note="putative"
320..943
/feature="SOD"
/note="similar to Mycobacterium tuberculosis superoxide
dismutase encoded by the sequence presented in GenBank
Accession Number X52861"
/codon_start=1
/transl_table=11
/product="superoxide dismutase"
/protein_id="AAC27527.1"
/db_xref="GI:3342172"
/translation="MAEYTLPLDMDYGLPEHISQINELHSHKHATYVKANDAV
AKLEBARAKEDHSAIILNEKNLAFNLAGHVNHTIMKNLSPNGDKPTGELAAIADA
FGSFDRKRAQFHAATTVQSGWALGMDTLGNKLLILOYVDHQINPELGIIVPLLLD
MMEHAFYLYQKVKVDFAKAFNVVVMADVQSRVAAATSTQKGLIFG"
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ORIGIN

Alignment Scores:

Pred. No.:	3,31e-07	Length:	943
Score:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	1	Gaps:	0

US-09-987-190-2 (1-30) x AF077406 (1-943)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20

Db 326 GAATPACACCTTGCCAGACTGAGACTGAGACGAGACTGGAACCGCACATCTCGGGT 385

QY 21 GlnIleasnGluIle***TyrThr 28

Db 386 CAGATCAACGAGCTTCACACAGC 409

RESULT 20

LOCUS AF061030 1321 bp DNA linear BCT 03-MAR-1999

DEFINITION Mycobacterium tuberculosis superoxide dismutase (sodA) gene,

ACCESSION AF061030

VERSION AF061030.1 GI:4321775

SOURCE Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

REFERENCE 1 (bases 1 to 1321)

AUTHORS Harth,G. and Horwitz,M.A.

TITLE Export of recombinant Mycobacterium tuberculosis superoxide dismutase is dependent upon both information in the protein and mycobacterial export machinery. A model for studying export of leaderless proteins by pathogenic mycobacteria

JOURNAL J. Biol. Chem. 274 (7), 4281-4292 (1999)

MEDLINE 99134360

PUBMED 9933629

REFERENCES 2 (bases 1 to 1321)

AUTHORS Harth,G. and Horwitz,M.A.

TITLE Direct Submission

JOURNAL Submitted (23-APR-1998) Medicine, UCLA, 10833 Le Conte Avenue, Los Angeles, CA 90095, USA

FEATURES

source 1..1321

/organism="Mycobacterium tuberculosis"

/mol_type="genomic DNA"

/strain="Hrdman"

/db_xref="taxon:1773"

542..1165

/gene="soda"

542..1165

/gene="soda"

/EC_number="1.5.1.1"

CDS

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/codon_start=1
/transl_table=11
/product="superoxide dismutase"
/protein_id="MAD15824.1"
/db_xref="GI:4321776"
/translation="MAEYTLPLDMDYGLPEHISQINELHSHKHATYVKANDAV
AKLEBARAKEDHSAIILNEKNLAFNLAGHVNHTIMKNLSPNGDKPTGELAAIADA
FGSFDRKRAQFHAATTVQSGWALGMDTLGNKLLILOYVDHQINPELGIIVPLLLD
MMEHAFYLYQKVKVDFAKAFNVVVMADVQSRVAAATSTQKGLIFG"
```

ORIGIN

Alignment Scores:

Pred. No.:	5.03e-07	Length:	1321
Score:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	1	Gaps:	0

US-09-987-190-2 (1-30) x AF061030 (1-1321)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20

Db 548 GAATPACACCTTGCCAGACTGAGACTGAGACGAGACTGGAACCGCACATCTCGGGT 607

QY 21 GlnIleasnGluIle***TyrThr 28

Db 608 CAGATCAACGAGCTTCACACAGC 631

RESULT 21

LOCUS AX708732 1321 bp DNA linear PAT 04-APR-2003

DEFINITION Sequence 57 from Patent WO02074991.

ACCESSION AX708732

VERSION AX708732.1 GI:29564462

SOURCE Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

REFERENCE 1

AUTHORS Karlson,F.

JOURNAL Detection of microorganisms using inducible genes

Patent: WO 02074991-A 57 26-SEP-2002;

Norchip A/S (NO)

FEATURES

source 1..1321

/organism="Mycobacterium tuberculosis"

/mol_type="unassigned DNA"

/db_xref="taxon:1773"

542..1165

/note="unnamed protein product"

/codon_start=1

/transl_table=11

/protein_id="CAD88162.1"

/db_xref="GI:29564463"

/db_xref="REMBTREMBL:CAD88162"

/translation="MAEYTLPLDMDYGLPEHISQINELHSHKHATYVKANDAV

AKLEBARAKEDHSAIILNEKNLAFNLAGHVNHTIMKNLSPNGDKPTGELAAIADA

FGSFDRKRAQFHAATTVQSGWALGMDTLGNKLLILOYVDHQINPELGIIVPLLLD

MMEHAFYLYQKVKVDFAKAFNVVVMADVQSRVAAATSTQKGLIFG"

Alignment Scores:

Pred. No.:	5.03e-07	Length:	1321
Score:	94.00	Matches:	15
Percent Similarity:	89.29%	Conservative:	10
Best Local Similarity:	53.57%	Mismatches:	3
Query Match:	64.83%	Indels:	0
DB:	6	Gaps:	0

US-09-987-190-2 (1-30) x AX708732 (1-1321)

```
Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSergly 20
Db 548 GAATACACCTTGCCACACCTGGACCTGGACCTACGAGACCTGGAACCGACATCTCGGGT 607
Qy 21 GlnIleasnGluIle***TyrThr 28
Db 608 CAGATCAACGACCTTCACACAGC 631

RESULT 22
AE007188 14282 bp DNA linear BCT 27-APR-2001
LOCUS Mycobacterium tuberculosis CDC1551, section 274 of 280 of the
DEFINITION complete genome.
ACCESSION AE007188 AE000516
VERSION AE007188.1 GI:13883836
KEYWORDS
SOURCE
ORGANISM
Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE
1 (bases 1 to 14282)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
Peterson,J., Deboy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
Kolonyak,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
Unpublished
2 (bases 1 to 14282)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
Peterson,J., Deboy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
Kolonyak,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
LOCATION/Qualifiers
1. 14282
/organism="Mycobacterium tuberculosis CDC1551"
/mol_type="genomic DNA"
/strain="CDC1551"
/db_xref="taxon:83331"
/note="clinical strain"
130..675
/gene="MT3949"
130..675
/gene="MT3949"
/note="similar to GB:AE000666, identified by sequence
similarity; putative"
/transl_table=1
/codon_start=1
/product="ferritin family protein"
/protein_id="AAK48316.1"
/db_xref="GI:13883837"
/translacion="MTEYEGPTKTPHALMOEJHNEFTAAQGVATAYVDSDDI
AKHFSQAVERNHAMLVQHILDRPLRYVPCVDYVRQFDRPRALALADQERTV
TDQVGLTAVARDEGDELGEQFMQWLFQBJEVALMATIVRADRAAGALFELNFV
AREVDVAPASGAPHAAGRL"
/complement(690..1520)
/gene="MT3950"
/complement(690..1520)
/note="similar to SP:P37965 GB:Z26522 PID:403373
GB:AU009126, identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="glycerophosphoryl diester phosphodiesterase,
putative"
/protein_id="AAK48317.1"

/dx_xref="GI:13883838"
/translacion="MDMTADVAVLAGHPFVVAHRAASARPHNTLAADIAKEGADG
VECDYRLDRDHGVCHVDRRLDRSTSGAGIVSTMTLADQLRELFYGMHDSNRPDSHG
DTSLLTDAIVSLVDHMRPKYKIFETHPVRYSGLVENKTLALHRTGLIAPASDR
SRAYVMSFAAIVRIIRAAPLLPTVLLGKPRYLTSSAATVGAATVAVGPSIPALKEY
FQLVDRSAQGRAYVCMNVDEVEDIDFCEVGVAMIGTHHPRTKAMJEDGRANGCTR"
/complement(1520..2548)
/gene="MT3951"
/complement(1520..2548)
/gene="MT3951"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK48318.1"
/db_xref="GI:13883839"
/translacion="MIQVCSQCGTGMVNERORVWCPCRCGLTAPLADMPAEARMT
PARQVPTASDTRTPRLPGFPMIAVRPGAAPPBPRGPRGTPRYAGIPRWGLT
DHVQAPVPASAKAGSPAAVATLLVSLVFSIAVVYFVRYVLITNNRTLLNSIV
ASAVMIGLVISLAIAAAGTTVLIVRMIVARRAAMPAGQEPBRSARLMAQCL
PMVNLIAPLVITLALVEDRYTLRRTIVVMVIVTASNISMFAFTSVVTAQGI
ANNTIMVLAIVCAAAVAAARVFEQKPRVBPARRVWVNTDGSAPASVAVE
LDQGEPPA"
2776..2880
/gene="MT3952"
2776..2880
/gene="MT3952"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK48319.1"
/db_xref="GI:13883840"
/translacion="MDNSARQVLIIDSLAGTRAKWIALSIHICPGCT"
3087..3236
/gene="MT3953"
3087..3236
/gene="MT3953"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK48320.1"
/db_xref="GI:13883841"
/translacion="MAHSTGPGSTTPPNSGPEWHAYGIALRALIALALIAIUA
VIALV"
complement(3637..3849)
/gene="MT3954"
complement(3637..3849)
/gene="MT3954"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK48321.1"
/db_xref="GI:13883842"
/translacion="MAIRVDLDSGRKASRPPIQDSFGLVDAGIGHAVTVEAELAK
ERLCGAVAGIAIPGLSDRAQVNO"
complement(4199..4801)
/gene="MT3954.1"
complement(4199..4801)
/gene="MT3954.1"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK48322.1"
/db_xref="GI:13883843"
/translacion="WTGDRKRVSDSDQPPADSWILGSHGALLCMEVLPFIVNHVL
MKSSRIPTQPTVAVRELVAGEPSYTLAPALPHRPRORSGSSRAAVLIVDDSMFH
PSTRRCALPQGHQFPKGGCFRRQSSWRSRSRAQTSRKRRALQPLRRPYLLTTTP
SRHYKRYKPKYKXASGRLPDQPVQCLTLTFAFRKQVP"
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gene      4727..5218
          /gene="MT3955"
CDS       4727..5218
          /gene="MT3955"
          /note="similar to GP:184145; identified by sequence
          similarity; putative"
          /codon_start=1
          /transl_table=11
          /product="TS1608", transposase"
          /protein_id="AAK48323.1"
          /db_xref="GI:13883844"
          /translation="MTAENPGRSRRTLVGIDAAITACHTAIRDVGARSIRSVSEPT
          LAGRTITDKLSGDDIDATVPEPTSMWLTITAVENAGDPTMAGARHCARLGATV
          GKSKSVIDAEVLTFRASEVDLPTLPTPAQALARSVRIRAGAVIDAKRSRRLMS
          LAR"
          complement(5255..5797)
          /gene="MT3957"
          /complement(5255..5797)
          /gene="MT3957"
          /note="identified by Glimmer2; putative"
          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
          /protein_id="AAK48324.1"
          /db_xref="GI:13883845"
          /translation="MGI:SKTIPRCRSLPLVGRGRRPSLRGDSITVTPCSPTMGK
          EPKMETASSDRCYCNRIPCRQMSACRFVYLVHVSQAVYVGVGVVGVQDQFPR
          AAGDRAVGVVAVQVGAAGDRHPGAFGLAGDGGELGVAMPDLSHQPVVERQVAG
          RCAGQADVGPTPOHRCRGR"
          5778..5993
          /gene="MT3958"
          5778..5993
          /gene="MT3958"
          /note="identified by Glimmer2; putative"
          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
          /protein_id="AAK48325.1"
          /db_xref="GI:13883846"
          /translation="MVPDKPTVSCLSVSHFORLFRVAOHNPVEYIRRDYHTQHLHD
          RDSGRRLTSSFAFPAPATQRHGS"
          complement(6207..6386)
          /gene="MT3959"
          complement(6207..6386)
          /gene="MT3959"
          /note="identified by Glimmer2; putative"
          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
          /protein_id="AAK48326.1"
          /db_xref="GI:13883847"
          /translation="WWRSGMGVGGKKSSTAQOLAGTANELTKREVLRAVHESPIVR
          DVVVIGIPAVDRRPFQ"
          6657..7280
          /gene="MT3960"
          6657..7280
          /gene="MT3960"
          /note="similar to SP:P47201 PID:555746 PID:620990
          PID:667039 SP:P53647; identified by sequence similarity;
          putative"
          /codon_start=1
          /transl_table=11
          /product="superoxide dismutase"
          /protein_id="AAK48327.1"
          /db_xref="GI:13883848"

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Alignment Scores:

Score:	Length:
94.00	14282
89.29%	15
53.57%	10
64.83%	3
	0
	0

DB: 1 Gaps: 0

```

US-09-987-190-2 (1-30) x AE007188 (1-14282)
Qy      1 LysTyrSerLeuProGluLeuAspTyrGluPhSerAlaThrGluProTyrIleSergly 20
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      6663 GAATACACCTTGCACCTGGACCTGGACTACGACGACCTGACACCGCACATCTCGGT 6722
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      21 GAlleAsnGluIle**TyrThr 28
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      6723 CAGATCAACGAGCTTCACCAACG 6746
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 23
BX842584      244800 bp      DNA      circular BCT 21-NOV-2003
Mycobacterium tuberculosis H37Rv complete genome; segment 13/13.
LOCUS      BX842584 AL021426 AL022076 AL022120 AL123456 280343 283864
DEFINITION      294121 297188
ACCESSION      BX842584.1 GI:38490370
VERSION      complete genome.
KEYWORDS      Mycobacterium tuberculosis H37Rv
SOURCE      Mycobacterium tuberculosis H37Rv
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
      Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
      tuberculosis complex.
REFERENCE
  1
    Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
    Harris,D., Gordon,S.V., Eigmeier,K., Gas,S., Barry III,C.E.,
    Tekala,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
    Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
    Hamlin,N., Holroyd,S., Hornsby,T., Tagatz,K., Krogh,A., McLean,J.,
    Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
    Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
    Squares,S., Squires,R., Sulston,D.E., Taylor,K., Whitehead,S. and
    Barrall,B.G.
    Deciphering the biology of Mycobacterium tuberculosis from the
    complete genome sequence
    Nature 393 (6685), 537-544 (1998)
    MEDLINE      98295987
    PUBMED      9634230
  2
    Camus,J.C., Pryor,M.J., Medigue,C. and Cole,S.T.
    Re-annotation of the genome sequence of Mycobacterium tuberculosis
    H37Rv
    Microbiology (Reading, Engl.) 148 (Pt 10), 2967-2973 (2002)
    MEDLINE      12368430
    PUBMED      12255591
  3 (bases 1 to 244800)
    Parkhill,J.
    Direct Submission
    Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
    tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
    Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
    Moleculaire Bacterienne, Institut Pasteur, 28 rue Ducreux Roux,
    75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
    On or before Nov 21, 2003 this sequence version replaced
    GI:3261511, GI:3256026, GI:3261558, GI:3261559, GI:3261648,
    GI:3261687, GI:3261736, GI:3261805.
    Notes:
    Details of M. tuberculosis sequencing at the Sanger Centre are
    available on the World Wide Web.
    (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/).
    FEATURES
    source
    1..244800
    /organism="Mycobacterium tuberculosis H37Rv"
    /mol_type="genomic DNA"
    /strain="H37Rv"
    /db_xref="taxon:83332"
    complement(89..1396)
    /locus_tag="RV3722c"
    complement(89..1396)
    /locus_tag="RV3722c"
    /function="UNKNOWN"
    /note="RV3722c, (MTV025.070c), len: 435 aa. Conserved

```

hypothetical protein, equivalent to 069513|MLCB2407.14
 alias 09CB73|ML2336, 463 aa) HYPOTHETICAL 46.8 KDA
 PROTEIN from Mycobacterium leprae (426 aa), FASTA scores:
 opt: 2505, E(): 8.3e-154, (87.25% identity in 424 aa
 overlap). Also highly similar to 09RU1|DR1579 CONSERVED
 HYPOTHETICAL PROTEIN from Deinococcus radiodurans (452
 aa), FASTA scores: opt: 1162, E(): 3.1e-67, (44.8%
 identity in 422 aa overlap); and partially similar to
 091371|PA1654 PROBABLE AMINOTRANSFERASE from Pseudomonas
 aeruginosa (388 aa) FASTA scores: opt: 162, E(): 0.0078,
 (25.85% identity in 348 aa overlap) and other
 aminotransferases. Tbpase score is 0.900. N-terminus
 extended since first submission (previously 408 aa)."
 /codon_start=1
 /evidence=experimental
 /transl_table=11
 /product="CONSERVED HYPOTHETICAL PROTEIN"
 /protein_id="CA18044.2"
 /db_xref="GI:38490371"
 /translation="MSFDSLSFQELIALAHSHQODYALQGMKALDLTRKPSAEQL
 DLSNQSLSPGDDVDRDPBGTDRNGYGHGLPGRLAIPAEILGIAVPLIAGNNSLE
 LMHDIVASMLYGVDSRPWIOEDGKICLPVGYDRHFAITETMGIEMLPIMLQ
 DGPVDLIEELVADPAIKGMWVVFNGNSGVTSMETVRIMOMTEADPDLFND
 NAYAVHTLIDPPOVDYGLAAKAGNPNRPYVASTSKITPAGGVSFPGSLGNTA
 WYLYAGKSTGPDKNQNRHLPFGADSRILMLRQQLARFPAIVAEVLQRLS
 ESKTASWTERKGVFISLDVTPGARRRVALAKOVGLAVTAGASFPYRKPDIDKNT
 IASFPSPVDLKNVVDGLATCALTAETILLNOGLASAPNVR"
 1613.1698
 /gene="tRNA-Ser (GGA)"
 1613.1698
 /locus_tag="RV3724B"
 /product="tRNA-Ser (GGA)"
 /note="codon recognized: UCC"
 /anticodon=(pos:1647..1649,aa:Ser)
 1804.2568
 /locus_tag="RV3723"
 1804.2568
 /locus_tag="RV3723"
 /function="UNKNOWN"
 /note="RV3723, (MTV025.071), len: 254 aa. Probable
 conserved transmembrane protein, with hydrophobic
 stretches at the N-terminus, and equivalent to
 069512|ML2337|MLCB2407.13c PUTATIVE MEMBRANE PROTEIN from
 Mycobacterium leprae (250 aa), FASTA scores: opt: 1029,
 E(): 1.2e-44, (64.45% identity in 253 aa overlap). Tbpase
 score is 0.900."
 /codon_start=1
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 /protein_id="CA18045.1"
 /db_xref="GI:2960147"
 /translation="MGRKVAVLMHASFISIGAVLYFYVLPWPELMGDTGHSIGTGL
 RIATGALVGLAIPVFTLIRKPELGTPOLASMLMSIMAHVLAGILVGTALSE
 VMLSLDAGOMLFGIYGAALAIIVLIGFFGYLSEVALPEPPKPLKPKPKRRLR
 KTKAGDEAPPEAPAEENETELAAQGBEVAVEPPESIESPGSPESATEAPAAETA
 TAEPKGLNRNRPPTGKTSRRRRRSGVAVAVE"
 2735.2977
 /gene="cut5a"
 2735.2977
 /locus_tag="RV3724A"
 2735.2977
 /gene="cut5a"
 /locus_tag="RV3724A"
 /EC_number="3.1.1.-"
 /function="HYDROLYSIS OF CUTIN (A POLYESTER THAT FORMS THE
 STRUCTURE OF PLANT CUTICLE)."
 /note="RV3724A, (MTV025.072), len: 80 aa. Probable cut5a,
 truncated cutinase precursor (EC 3.1.1.-), similar to
 N-terminal end of others e.g. 09K87 SERINE ESTERASE
 CUTINASE from Mycobacterium avium (220 aa), FASTA scores:
 opt: 202, E(): 1.5e-06, (56.45% identity in 62 aa
 overlap); 09XB09|RV22-RV1758 PROTEIN (FRAGMENT) from
 Mycobacterium bovis BCG (143 aa), FASTA scores: opt: 200,
 E(): 1.5e-06, (61.4% identity in 57 aa overlap); and

000298|CUTI BOTCI|CUTA CUTINASE PRECURSOR from Botrytis
 cinerea (Botryotinia fuckeliana) (202 aa), FASTA scores:
 opt: 108, E(): 2.2, (40.4% identity in 52 aa overlap).
 Also highly similar to others from Mycobacterium
 tuberculosis e.g.
 006318|CUTI MYCTU|RV3451|MT3557|MTCY13E12.04 PROBABLE
 CUTINASE PRECURSOR (247 aa), FASTA scores: opt: 189, E():
 1.2e-05, (58.0% identity in 50 aa overlap);
 050664|CUTI MYCTU|RV2301|MT3358|MTCY339.08c PROBABLE
 CUTINASE PRECURSOR (219 aa), FASTA scores: opt: 172, E():
 0.00015, (59.2% identity in 49 aa overlap);
 006793|RV1758|MTCY28.24|Z95890 HYPOTHETICAL 17.9 KDA
 PROTEIN (174 aa), FASTA scores: opt: 641, E(): 2.7e-29,
 (57.2% identity in 166 aa overlap);
 006319|RV3452|MTY13E12.05, and U00015.11 from Mycobacterium
 leprae. BELONGS TO THE CUTINASE FAMILY. Rest of cutinase
 ORF continues as RV3724B|CUT5B, frameshifting could occur
 near position 416968. Sequence has been checked but no
 errors found."
 /codon_start=1
 /transl_table=11
 /product="PROBABLE CUTINASE PRECURSOR [FIRST PART] CUT5A"
 /protein_id="CAE55632.1"
 /db_xref="GI:38490372"
 /translation="MDVIRMARRLAAVAGTAATVTPGLLSAHVPMWSAECPDVEV
 PARCTGPPGIGSGVGLFVDALRPPGRQVTRGLRR"
 2874.3437
 /gene="cut5b"
 /locus_tag="RV3724B"
 2874.3437
 /locus_tag="RV3724B"
 /EC_number="3.1.1.-"
 /function="HYDROLYSIS OF CUTIN (A POLYESTER THAT FORMS THE
 STRUCTURE OF PLANT CUTICLE)."
 /note="RV3724B, (MTV025.072), len: 187 aa. Probable cut5b,
 truncated cutinase (EC 3.1.1.-), similar to C-terminal end
 of others e.g. 09XB09|RV22-RV1758 PROTEIN (FRAGMENT) from
 Mycobacterium bovis BCG (143 aa) FASTA scores: opt: 335,
 E(): 3.4e-12, (53.25% identity in 92 aa overlap); 09K87
 SERINE ESTERASE CUTINASE from Mycobacterium avium (220
 aa), FASTA scores: opt: 251, E(): 2.5e-07, (44.05%
 identity in 168 aa overlap). Also similar to proteins from
 Mycobacterium tuberculosis e.g. 006793|RV1758|MTCY28.24
 HYPOTHETICAL 17.9 KDA PROTEIN (174 aa), FASTA scores: opt:
 641, E(): 2.5e-29, (57.25% identity in 166 aa overlap);
 006319|RV3452|MTCY13E12.05 HYPOTHETICAL 23.1 KDA PROTEIN
 (226 aa), FASTA scores: opt: 385, E(): 7.5e-15, (46.65%
 identity in 165 aa overlap);
 006318|CUTI MYCTU|RV3451|MT3357|MTCY13E12.04 PROBABLE
 CUTINASE PRECURSOR (247 aa), FASTA scores: opt: 307, E():
 1.9e-10, (40.7% identity in 167 aa overlap);
 Q10837|CUTI MYCTU|RV1984c|MT2037|MTCY39.35 PROBABLE
 CUTINASE PRECURSOR (217 aa), FASTA scores: opt: 261, E():
 6.7e-08, (50.9% identity in 169 aa overlap); etc; and
 U00015.11 from Mycobacterium leprae. 5'-end of gene is
 RV3724A|CUT5A, frameshifting may occur near position
 416968. Tbpase score is 0.918."
 /codon_start=1
 /transl_table=11
 /product="PROBABLE CUTINASE (SECOND PART) CUT5B"
 /protein_id="CAE55633.1"
 /db_xref="GI:38490373"
 /translation="MAPGSHLVLAASEDCGSHCVSGQAKSLGVAANYNPASNDPAS
 SDPKVVDIGINDAGSHIGSMASCPQTSQVGGQGAADVATSAVVPAPVQVA
 VAPAPAEVANAIVAAVTLFGAPSAQPLGAGAPPIAIGPLHYCKTQLCADGDSICGD
 GNSPVAHGIVAAVWGQGANFAASRL"

Alignment Scores:
 Pred. No.: 0.000327 Length: 244800
 Score: 94.00 Matches: 15
 Percent Similarity: 89.29% Conservative: 10
 Best Local Similarity: 53.57% Mismatches: 3

LVAGTQYIVNALDLRLAKAPGDLIVAPTSRTTALPOLRIIAASPNQPNCTLR
 EANRAGSVOMGSDPYATGDI.VLTSVCGAAYRRARERTITVVGSSNFMNGLLP
 AGNALAMNLACNPRILWYADPHIEGKSSSSJDLIPENWHTIWLQMLVLLVA
 LMKGRIGPLVVEEPVIRASETVEGRRLYRRARRADALRTATLQCLRLRLG
 VGAGAPAPVAVVTIQRSKADPPFVAHYLFGAPATDNDLQLARALDDIERQVHS"
 3863. .4939
 /gene="moxr2"
 /locus_tag="Mb3717"

CDS

3863.4939
 /gene="moxr2"
 /locus_tag="Mb3717"
 /note="Mb3717, moxR2, len: 358 aa. Equivalent to Rv3692, len: 358 aa, from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 358 aa overlap). Probable moxR2, methanol dehydrogenase regulatory protein, highly similar (generally longer at N-terminus) to Q9KYM3|SCE33.20 PUTATIVE REGULATORY PROTEIN from Streptomyces coelicolor (329 aa), FASTA scores: opt: 1523, E(): 4.2e-74 (70.9% identity in 330 aa overlap); Q9Z538|SC9B2.21c PUTATIVE REGULATORY PROTEIN from Streptomyces coelicolor (332 aa) FASTA scores: opt: 1008, E(): 1.1e-46 (50.8% identity in 313 aa overlap); Q9U267|MOXR-3|PAB0848 METHANOL DEHYDROGENASE REGULATORY PROTEIN from Pyrococcus abyssi (314 aa), FASTA scores: opt: 989, E(): 1.1e-45 (50.6% identity in 302 aa overlap); Q9AAN1|CC0566 MOXR PROTEIN from Caulobacter crescentus (323 aa), FASTA scores: opt: 988, E(): 1.3e-45 (52.3% identity in 306 aa overlap); etc. Also similar to O53170|MTV007.26|MOXR|Fv1479 from Mycobacterium tuberculosis (377 aa); and O07392|AF002133.6|MOXR from Mycobacterium avium (309 aa). Also high similarity with several hypothetical bacterial proteins."

gene

CDS

/codon_start=1
 /transl_table=1
 /product="PUTATIVE METHANOL DEHYDROGENASE TRANSCRIPTIONAL REGULATORY PROTEIN MOXR2"
 /protein_id="CAD95903.1"
 /db_xref="GI:31620461"
 /translation="MTQSASNPQAPPTQTGALPGYPPQAGAPTAAPSGPHPRAE
 AESARDALMLRAEVAWVGQDGVISGLVIALCRGHVLEGGVGAKTLLIYAMA
 ALQLEFRVQFTPLMPGDVGSIVYDARVAEVEFRGPVPTNLLADLNRPKTKO
 AALLMEERQVSEEGPKPLNPFIVAATONPLEVGTGLOPAQOCDRLINVTIL
 PARDSEIATIDRAHAGFDPDLSINVAAPAEIAAGRAEVRHIVANEVYGVIVDI
 GATRSSPALQGVSPRCAITLIGTARSWMLSGRDVTPDVAKAMPETLRHRMLRP
 EAELEGATPDGVDGIIASVPPR"
 5073. .6395
 /locus_tag="Mb3718"
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 /locus_tag="Mb3718"
 /note="Mb3718, len: 440 aa. Equivalent to Rv3693, len: 440 aa (alternative start at 41910), from Mycobacterium tuberculosis strain H37Rv, (100.0% identity in 440 aa overlap). Possible conserved membrane protein, similar to Q9KYM2|SCE33.21 PUTATIVE LIPOPROTEIN from Streptomyces coelicolor (436 aa), FASTA scores: opt: 875, E(): 3.3e-46 (56.25% identity in 448 aa overlap); Q9AAN0|CC0567 HYPOTHETICAL PROTEIN from Caulobacter crescentus (437 aa), FASTA scores: opt: 355, E(): 2.3e-14 (30.9% identity in 450 aa overlap); P73233|SLR2013 HYPOTHETICAL 48.5 KDA PROTEIN from Synecocystis sp. strain PCC 6803 (435 aa), FASTA scores: opt: 340, E(): 1.9e-13 (29.7% identity in 438 aa overlap); etc. Equivalent to AAK48162 from Mycobacterium tuberculosis strain CDC1551 (475 aa) but shorter 35 aa. Also similar to other hypothetical proteins from Mycobacterium tuberculosis; MTV014_7, MTV007_27, and MTCY71_36 M."

/codon_start=1
 /transl_table=1
 /product="POSSIBLE CONSERVED MEMBRANE PROTEIN"

Alignment Scores:
 Pred. No.:
 Score:

0.000383 Length: 278492
 94.00 Matches: 15

Percent Similarity: 89.29%
 Best local Similarity: 53.57%
 Query Match: 64.83%
 DB: 1
 Gaps: 0

US-09-987-190-2 (1-30) x BX248347 (1-278492)

QY

1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrTlleSerGly 20

Db

189983 GAATACACTTCCCGACCTGACTGGAGCACTGGAACCGACATCTCGGDT 190042

QY

21 GlnIleAngIuile**TyrThr 28

Db

190043 CAGATCAACGAGCTTCACCAACAGC 190066

RESULT 25

LOCUS

PFSD 567 bp DNA linear BCT 14-MAR-1996

DEFINITION

P.freudenreichii sod gene (partial).

ACCESSION

X91650.1 GI:1061201

KEYWORDS

sod gene, superoxide dismutase.

SOURCE

Propionibacterium freudenreichii

ORGANISM

Bacteria; Actinobacteria; Actinobacteridae; Propionibacteriaceae; Propionibacterium.

REFERENCE

1 Gabbianelli R., Battistoni A., Pollio F., Carri M.T., De

AUTHORS

Mattino A., Meier B., Desideri A. and Rotilio G.

TITLE

Metal uptake of recombinant cambialistic superoxide dismutase from

JOURNAL

Propionibacterium shermanii is affected by growth conditions of

REMARK

host Escherichia coli cells

FEATURES

Biochem. Biophys. Res. Commun. 216 (3), 841-847 (1995)

source

1.567 /organism="Propionibacterium freudenreichii"

gene

/mol_type="genomic DNA"

CDS

/strain="P23"

gene

/sub_species="shermanii"

CDS

/db_xref="taxon:1744"

gene

1.567 /gene="sod"

CDS

1.567 /gene="sod"

gene

/EC_number="1.15.1.1"

CDS

/codon_start=1

gene

/transl_table=11

CDS

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gene

/protein_id="CA62838.1"

CDS

/db_xref="GI:1061202"

gene

/db_xref="GOA:Q59673"

CDS

/translation="MAVYTLPELPYQSYALPEYSGEIMELHDKKHKAAYVDCANTL
 DKLAERDKADGATINKLEKDLAFNAGHVNVSFVKMAPKSAARPRDEGAID
 EFGSGDKNAKQPTAAATIGSGMASLYWDPGRKINTLQFYDHNNLPAGSIPILQ
 LDMWEHAFYLTQIKYAGDYVKSMMNVVN"

ORIGIN

Alignment Scores:
 Pred. No.: 6.2e-07 Length: 567
 Score: 91.00 Matches: 16
 Percent Similarity: 84.62% Conservative: 6
 Best local Similarity: 61.54% Mismatches: 4
 Query Match: 62.76% Indels: 0
 DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x PFSSOD (1-567)

QY 2 TyrsenleuprogluLeuaspTyrgluPheSerAlaThrGluProTyrIleSerglycIn 21
 10 TACACGCTGCCGGAACCTTCCTACGACTACTCGGCCCTGAGCCGATACATCTCGGGTGAG 69

Db 22 IleasnGluIle***Tyr 27
 70 ATCATGAGCTCCACCAT 87

RESULT 26

PFSSOD 567 bp DNA linear BCT 15-MAY-1998
 LOCUS P.friedenreichii sod gene, partial.
 DEFINITION Y09012
 VERSION Y09012.1 GI:3135855
 KEYWORDS cytoplasmatic protein; sod gene; superoxide dismutase.
 SOURCE Propionibacterium freudenreichii
 ORGANISM Propionibacterium freudenreichii
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Propionibacteriaceae; Propionibacterium.

REFERENCE 1
 AUTHORS Gabblanelli, R., Battistoni, A., Polizio, F., Carri, M.T., De Martino, A., Meier, B., Desideri, A. and Rotilio, G.
 TITLE Metal uptake of recombinant cambariastic superoxide dismutase from host Escherichia coli cells
 JOURNAL Biochem. Biophys. Res. Commun. 216 (3), 841-847 (1995)

MEDLINE 96074560
 PUBMED 7488202
 2 (bases 1 to 567)
 Gabbianelli, R.
 TITLE Direct Submission
 SUBMITTED (24-OCT-1996) R. Gabbianelli, Dept. of Biology,
 University Tor Vergata, Via Della Ricerca Scientifica, Rome, ITALY

FEATURES
 Location/Qualifiers
 1..567
 /organism="Propionibacterium freudenreichii"
 /mol_type="genomic DNA"
 /strain="P23"
 /sub_species="Shermanii"
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 1..567
 /gene="sod"
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 /transl_table=1
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 /protein_id="CA70215.1"
 /db_xref="GI:3135855"
 /db_xref="GOA:O59673"
 /db_xref="SPTRMBL:O59673"
 /translation="MAVYTLPLRPDYALPEYISGETMELHHKHKAYVDGNTAL
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 LDMEHAFYLYQKNYKGDYVXSWNVVM"

gene
 CDS

ORIGIN
 Alignment Scores:
 Pred. No.: 6.2e-07 Length: 567
 Score: 91.00 Matches: 16
 Percent Similarity: 84.62% Conservative: 6
 Best Local Similarity: 61.54% Mismatches: 4
 Query Match: 62.76% Indels: 0
 DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x PFSSOD (1-567)

QY 2 TyrsenleuprogluLeuaspTyrgluPheSerAlaThrGluProTyrIleSerglycIn 21
 10 TACACGCTGCCGGAACCTTCCTACGACTACTCGGCCCTGAGCCGATACATCTCGGGTGAG 69

Db 10 TACACGCTGCCGGAACCTTCCTACGACTACTCGGCCCTGAGCCGATACATCTCGGGTGAG 69
 QY 22 IleasnGluIle***Tyr 27
 70 ATCATGAGCTCCACCAT 87

RESULT 27
 AEO16851 302529 bp DNA linear BCT 11-AUG-2003
 LOCUS Tropheryma whipplei str. Twist, section 2 of 3 of the complete genome.
 DEFINITION AEO16851 GI:28476223
 ACCESSION AEO16851.1 GI:28476223
 VERSION AEO16851.1
 KEYWORDS Tropheryma whipplei str. Twist
 SOURCE Tropheryma whipplei str. Twist
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Micrococcineae; Cellulomonadaceae; Tropheryma.

REFERENCE 1
 AUTHORS Raoult, D., Ogata, H., Audic, S., Robert, C., Sultre, K., Drancourt, M. and Claverie, J. M.
 TITLE Tropheryma whipplei Twist: A Human Pathogenic Actinobacteria With a Reduced Genome
 JOURNAL Genome Res. 13 (8), 1800-1809 (2003)

MEDLINE 22784088
 PUBMED 12902375
 2 (bases 1 to 302529)
 Raoult, D., Audic, S., Robert, C., Ogata, H., Sultre, K., Drancourt, M. and Claverie, J. M.
 TITLE Direct Submission
 SUBMITTED (26-JUL-2002) Unite des Rickettsies, Faculte de Medecine,
 CNRS UMR 6020, IFR 48, Universite de la Mediterranee, 27 boulevard
 Jean Moulin, Marseille Cedex 05 13385, France

FEATURES
 Location/Qualifiers
 1..302529
 /organism="Tropheryma whipplei str. Twist"
 /mol_type="genomic DNA"
 /strain="twist"
 /db_xref="taxon:203267"
 /complement (170..1975)
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 /locus_tag="TW216"
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 /EC_number="2.7.1.-"
 /codon_start=1
 /transl_table=1
 /product="serine/threonine-protein kinase"
 /protein_id="AA044313.1"
 /db_xref="GI:28476224"

gene
 CDS
 /translation="MRDASVIGMRIDRVLITKIASGMAVYKGDILKRDVSI
 KIMDHVNDPKPTKEKPIAEKQIAGISNAINVAVPDGRKNRIAYMMERYVPTLR
 KLNRKVLVYKQTLLEITTCYBELGSNHRKGLHDKPNNITLIGNGOKIKGPGI
 SRLSNNTTGTGLGTAIVSPDLIRSEADTSDVAITGIMFELITGQOPREGKO
 PMEVAHKKANLPMKPSANVPGVPSVDIVLMACSKNPEKPSDASVLAALAKKINL
 ENKSTIDATEIILIDFGASENLKTPQKMIKILVAVILPVLVSGSVFPLAAGP
 STVETIDAGLTPRIKLEKGLVITISQKYDVSQGIINLPSAGTMBERKTL
 ELDSISGRVDPDIAGLPISEALSLIRDDIKIROEHSQSGGLVIVSVYKKS
 GDDISHGGRVSENDLITLSSIGALPNIIGMBEDAKALNAGLAVALIOENDVY
 PKGRVIRQTPSGDPTVKGSAINFAVSKGPDIVYPNLTGKTLHDAVDLTSLGPRVYL
 TTSIPLDARPAKIIITPSAGTAVKGRSVTVTPG"

gene

CDS

complement (1985..3124)
 /gene="idsA"
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 /locus_tag="TW217"
 /codon_start=1
 /transl_table=1
 /product="geranylgeranyl pyrophosphate synthase"
 /protein_id="AA044314.1"
 /db_xref="GI:28476225"


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QY      2  TyrsLeuProGluIleuAspTyrGluIleuSerAlaThrGluIleuProTyrIleuSerGlyIle 21
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      85496  TATACCTCCCTCATCGCTTATTCGTTATTCGTTAGAGCCCTATATTAAGGGGAAAA 85555
QY      22  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      85556  ATCATGAGCTTCATCACTCA 85576

RESULT 28
LOCUS   BX251411.c
DEFINITION Tropheryma whipplei TW08/27, complete genome; segment 2/3.
ACCESSION BX251411 BX072543
VERSION   BX251411.1 GI:28410574
KEYWORDS  complete genome.
SOURCE    Tropheryma whipplei TW08/27
           Tropheryma whipplei TW08/27
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Micrococciaceae; Cellulomonadaceae; Tropheryma.
REFERENCE
AUTHORS  Bentley,S.D., Maitland,M., Murphy,L.D., Pallen,M.J., Yeats,C.A.,
          Dover,L., Norbertczak,H.T., Besta,G.S., Quail,M.A., Harris,D.E.,
          von Herbay,A., Goble,A., Rutter,S., Squares,R., Squares,S.,
          Barrett,B.G., Parkhill,J. and Relman,D.A.
          Sequencing and analysis of the genome of the Whipple's disease
          bacterium Tropheryma whipplei
          Lancet 361, 627-634 (2003)
          2 (bases 1 to 299050)
          Bentley,S.D.
          Direct Submission
          Submitted (10-FEB-2003) Submitted on behalf of the Pathogen
          Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus,
          Hinxton, Cambridge CB10 1SA E-mail: sds@sanger.ac.uk
          location/Qualifiers
FEATURES
source    1..299050
           /organism="Tropheryma whipplei TW08/27"
           /mol_type="genomic DNA"
           /strain="TW08/27"
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           /db_xref="taxon:218496"
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           /locus_tag="TW287"
           /locus_tag="TW287"
           /note="Similar to Mycobacterium tuberculosis
           isolate Y1-CRNA synthetase Iles or Rv1536 or mlt1587 or
           mtcy48.29C SMALL:SYI_MycTU (SMALL:Q10765) (1041 aa) fasta
           scores: E(): 0, 52.58% id in 1046 aa, and to
           Methanoscarcina barkeri isolate Y1-CRNA synthetase Iles
           SMALL:Q9P919 (EMBL:AF208389) (1058 aa) fasta scores: E():
           3.3e-65, 30.23% id in 1065 aa"
           /codon_start=1
           /transl_table=11
           /product="class I tRNA synthetase (I, L, M and V)"
           /protein_id="CAD66961.1"
           /db_xref="GI:28410575"
           /translation="WCDOGFEVSSQSSNDYKQKORPFRPNLPKIEBSVLAFWSPDKTFE
           ASLEQRQGRKRVFTDGPFRANGFLPHRHILTGKDAIIPRYQIMRGQYVVRWMDT
           HGLPELEAMKRLGITKESQIESWGIAFNEAKRSKYTIYDQMEHYNNRQARVDRK
           NGYKTLDDYVESVLMARFLLYKKGVIEGKVLPCWDDQTPLSHLELRKLDDEVYKQ
           RLDDSLVTVPFLIQGKAKTCGIDGVALALMTTPWTLPSNMAIIVSPNVEYVVSAR
           QNSNSDFLCKSLSDYVACLGYESGODARASIRRTLLKEIGIHYPLDYVADLR
           NAFITLSNYDVNTRGTCGIVASPAHGGDDKRVCAFGVPTVASINDAACGFDVSNY
           AGMHLFDANAVTRSLSDGRLLRHSRKHSPHWRKRSPLIYKAVTSWSPRITDSY
           NRMLELNQIIMWPKSVKNGQFALMSAKDSISRTRWGTFIYWKSNDEYTRID
           CYSLKELEDGFGILKTLDRBEIDRLTRPNDDPTGASTYMRKRPVDPVADWEDASMP
           FAOLHYPENIERPEANKSADIEVAGQIRGMFYLLHAMSALDGVAFKALDHGI
           VUGDGGKASKSLRNYPDVYVFNENGGPAVWYLISSILRGSGLIYSRKKIQAIR
           CYTTPKSSWTFRHHYTSRAAPRGYKARPSVDCIILRYSILSKGLIYEDVTRFMS
           FDMASALQLRDFAVLTWYTRSRDRFWDSDTGAPRTIYVETICRGAVVPM
           VSEHYKHTIINSRVSLSDWPDVATFPNETGIVETMDRKYCTGLSKRLKGLIKAR
           OPLSASHIRVAVQVSLAQYKDIISGLINVTYSIEGSCQYRMKLTLPVAPRPLAGD
           VQTVIAARGDWTHDGHVTAIGIPLIENEQVLVAGADSPNSPLPFGGSDVITDTR
           IDETLRSGVADTYRQIOIAKENDLNTTRISLEVCPDQVKNMILAFSELICKE

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misc_feature 174..2094
           /locus_tag="TW287"
           /note="tRNA synthetases class I (I, L, M and V) Score =
           626.0 E-value = 1.5e-185"
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           /gene="tfs"
           /locus_tag="TW288"
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           /gene="tfs"
           /locus_tag="TW288"
           /EC_number="6.3.2.17"
           /note="Similar to Lactobacillus casei folypolylglutamate
           synthase Fgs SMALL:POLC_LACCA (SMALL:P15925) (428 aa)
           fasta scores: E(): 6.4e-22, 33.23% id in 343 aa, and to
           Corynebacterium glutamicum folypolylglutamate synthase
           cg12375 SMALL:BA099768 (EMBL:AP005281) (458 aa) fasta
           scores: E(): 5.6e-47, 37.14% id in 455 aa"
           /codon_start=1
           /transl_table=11
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           /protein_id="CAD66962.1"
           /db_xref="GI:28410576"
           /translation="WSRAGRALDQPRLDGKYLALSYLSNPQCAPVHINGTKTV
           SRMIACILSLRVLGLFSPHITALEERIQIDMNPVQHTLEKMFIDFQRLADA
           HLEKKNCPPLTFEFCMTVLAFCSDPTVDVWLEVGAMQADATNVADRVCPET
           DFDHGRIGRLERIEIAHTKAGIKPSPFVVAASQHVQCELDYFASINIGQSYDT
           ELDDKIRFGQDPCQYKPVAGGQIDLRGLYGECEVFLPLFGYQAKRNALIAIV
           ESFGRVREHIVLEARSNTSPGRLOISKNPVLLDAAHPHAKLALALDEFFSF
           GKIVFIATLSDQIDBSIINLMSFLHGSIRVTSDSYSEBSRSTRSNRVFVITQ
           STPRVAVAQVAFSIAKRVANBGLIVCESANDAFQYSTRLPDAIVVSGISILISF
           IPR"
           /gene="fsg8"
           /gene="fsg8"
           /locus_tag="TW288"
           /note="Mur ligase family, catalytic domain Score = 34.0
           E-value = 1.1e-07"
           /gene="fsg8"
           /gene="fsg8"
           /locus_tag="TW288"
           /note="PSP01011 Polylipolylglutamate synthase signature 1."
           /locus_tag="TW288"
           /gene="fsg8"
           /locus_tag="TW288"
           /locus_tag="TW288"
           /note="PSP01012 Polylipolylglutamate synthase signature 2."
           /gene="fsg8"
           /locus_tag="TW288"
           /locus_tag="TW288"
           /note="Mur ligase family, glutamate ligase domain Score =
           27.3 E-value = 2.6e-05"
           /locus_tag="TW289"
           /locus_tag="TW289"
           /locus_tag="TW289"
           /locus_tag="TW289"
           /locus_tag="TW289"
           /note="Similar to Streptomyces coelicolor putative
           membrane protein SCO2613 or SCO88.24C SMALL:O9J1G5
           (EMBL:AL139298) (118 aa) fasta scores: E(): 0.83, 28.84%
           id in 104 aa"
           /codon_start=1
           /transl_table=11
           /product="putative membrane protein"
           /protein_id="CAD66963.1"
           /db_xref="GI:28410577"
           /translation="WNYLRKTVARVLSFELVAFILAGVFLTFMPFDRFPDGIFIAV
           VPMAFLALISLSKLFGLITGMIVQIFITVGFISIPAIKFGTFGLMAYALMSARH
           HNGHRQC"
           /locus_tag="TW289"
           /locus_tag="TW289"
           /note="Signal peptide predicted for Unknown_CDS by SignalP
           2.0 HMM (Signal peptide probability 0.899) with cleavage
           site probability 0.318 between residues 60 and 61;
           signal-peptide site"
           order(4760..4813,4841..4909,4946..5014)
misc_feature

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/misc_feature /locus_tag="TW289"
                /note="3 probable transmembrane helices predicted for
                unknown_CDS by TMHMM2.0 at aa 12-29, 39-61 and 74-96"
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                /gene="ndk"
                /locus_tag="TW290"
                5121..5531
                /gene="ndk"
                /locus_tag="TW290"
                /EC_number="2.7.4.6"
                /note="Similar to Streptomyces coelicolor nucleoside
                diphosphate kinase Ndk or SCO2612 or SCC88.23C
                SMALL:NDK_STRCO (SMALL:P50589) (137 aa) fasta scores: E():
                5.6e-23, 48.52% id in 136 aa, and to Dictyostelium
                discoideum nucleoside diphosphate kinase, cytosolic NdkB
                or NdkC or Gipi7 SMALL:NDKC_DICDI (SMALL:P22887) (155 aa)
                fasta scores: E(): 3e-24, 46.5% id in 134 aa"
                /codon_start=1
                /transl_table=11
                /product="nucleoside diphosphate kinase"
                /protein_id="CAD66964.1"
                /db_xref="GI:28410578"
                /translation="MECTLVIIKPDGIRGLIGVLRIEAKGYQIVDIRMLVDDROS
                VEHYLHRDRHFPYLPVDMTSGPIVVRAGGVVDALKTIVGVSPTTLALPGTTR
                GDFGRNMGIDVYQNI VHASDSVSKAKRELDIMP"
                5124..5526
                /gene="ndk"
                /locus_tag="TW290"
                /note="Nucleoside diphosphate kinase Score = 164.4 E-value
                = 1.3e-46"
                5466..5492
                /gene="ndk"
                /locus_tag="TW290"
                /note="PS00469 Nucleoside diphosphate kinases active
                site."
                5749..7398
                /gene="rnc"
                /locus_tag="TW291"
                5749..7398
                /gene="rnc"
                /locus_tag="TW291"
                /EC_number="3.1.4.-"
                /note="Similar to Escherichia coli ribonuclease E Rne or
                Ams or Hmp1 or h1084 SMALL:RNE_ECOLI (SMALL:P21513) (1061
                aa) fasta scores: E(): 9.7e-38, 36.25% id in 411 aa, and
                to Streptomyces coelicolor hypothetical protein SCO2599 or
                SCC88.10C SMALL:O9LIH8 (EMBL:AL139298) (1340 aa) fasta
                scores: E(): 1.6e-58, 44.28% id in 560 aa"
                /codon_start=1
                /transl_table=11
                /product="ribonuclease E"
                /protein_id="CAD66965.1"
                /db_xref="GI:28410579"
                /translation="MFGRCMVNDGSKRAGCYKVFQAPDPSSARIVSQKRSDDTPTRQ
                SKRRASRTSPAFETGLLRNTRQPMYLRGSSASVQVGLIEGLIVEYVARGSSSLV
                GNITMRGVQVLDLGMELAFYDIDCGRNAVLYSEAVGYSRIASEPRAIRLOKSLAAVEDSS
                VTDAAVANKSPRTQGLSLAGRYLVAAPGSGVSRIRASERARLQKSLAAVEDSS
                LIIRTAAGVATISFQLGNDAKMLCEAVRAIKERKENATAPSIITSEPDLLIRLDREN
                NDFKELIVEGALYERVNSYLQDVSEPMGKVSSEEDIFDARYTTEOIRSLINKY
                LPSGSLVVDHTEAMTVITDNTGKFEVSSSEIQQVTVDDNNLEAVETIRQIRLDLG
                GIVYIDFIMLLOENRDVYNNRLLEALSIDRSHKAEITSLVLTQTKRKGVALEP
                VETLCRCGSGRGVIVPEPKPARKKRRRQVNAKASDAVAAYIISAMODTAGYSDAR
                SPTLSRGALAPRQSVSISVGNRRRLVTSTIDASDPRAS"
                7522..7836
                gene
                Alignment Scores:
                Pred. No.: 0.0643
                Score: 82.00
                Percent Similarity: 77.78%
                Best Local Similarity: 55.56%
                Query Match: 56.55%
                DB: 1
                Length: 299050
                Matches: 15
                Conservative: 6
                Mismatches: 6
                Indels: 0
                Gaps: 0

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US-09-987-190-2 (1-30) x BX251411 (1-299050)
QY 2 TyrsLerLupProGluLeuAspIyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 183212 TATACATCCCTTAATCTGCCTTATCTGCTTACGACCTCATATTAACGCGAAMA 183213
QY 22 IleAsnGluIle**TyrThr 28
Db 183212 ATTCAGAGAGCTTCACTCA 183192
RESULT 29
AB079877 655 bp mRNA linear INV 19-FEB-2002
LOCUS AB079877
DEFINITION Marsupinaeus japonicus sod-1 mRNA for superoxide dismutase like
protein, complete cds.
ACCESSION AB079877
VERSION AB079877.1 GI:18700488
KEYWORDS
SOURCE
ORGANISM
Marsupinaeus japonicus
Marsupinaeus japonicus
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Marsupinaeus.
REFERENCE
1 Soma,G., Inagawa,H., Nishizawa,T., Honda,T., Nomura,Y., Uenobe,M.,
Takahashi,Y., Itami,T. and Yokomizo,Y.
Takuma shrimp cDNA similar to superoxide dismutase protein
2 (bases 1 to 655)
Soma,G., Inagawa,H., Nishizawa,T., Honda,T., Nomura,Y., Uenobe,M.,
Takahashi,Y., Itami,T. and Yokomizo,Y.
Direct Submission
JOURNAL
Submitted (15-FEB-2002) Hiroyuki Inagawa, Tokushima Bunri
University, Institute for Health Sciences, Yamashiro-cho
Nishihama-bouji, Tokushima, Tokushima 770-8514, Japan
(E-mail:pina@tokushima.bunri-u.ac.jp, Tel:81-88-622-9611(ex.1104),
Fax:81-88-622-3217)
COMMENT
This study was supported by Grant-in-Aid of Recombinant Cytokine's
Project provided by the Ministry of Agriculture, Forestry and
Fisheries, Japan (RCP2001-2230).
FEATURES
source
1..655
/organism="Marsupinaeus japonicus"
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/protein_id="BAB85211.1"
/db_xref="GI:18700489"
/translation="MAEAKAYISIDEKLAELTGLIEVDQIKKNOPANADBAVAIRE
MATYVEGIVVQAGVAGVAGVQIQOMFQINVAIEIIEGEGALALPLIKYDPALEPH
ISMIMEIHHTGHOGYINILIAATKIVIAEALNAYVSANMALPLAIKNGGGHINT
IWTNAPDAGBEPQALIQALIDESIDHSVPQGFSAASVE"
ORIGIN
Alignment Scores:
Pred. No.: 7.48e-05
Score: 80.00
Percent Similarity: 77.78%
Best Local Similarity: 55.56%
Query Match: 55.17%
DB: 3
Length: 655
Matches: 15
Conservative: 6
Mismatches: 6
Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AB079877 (1-655)
QY 2 TyrsLerLupProGluLeuAspIyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 290 CATGCTGTCGCCCTCTCAAGTACGACTTAATGCGCTCGAAGCACACATTTCGGGCATG 349

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QY 22 lileasngluile***TyrThr 28
 DB 350 ATCATGAGATCATCATCACC 370
 RESULT 30
 LOCUS AB001693
 DEFINITION Equus caballus Mn-SOD mRNA for manganese superoxide dismutase,
 complete cds.
 ACCESSION AB001693.1 GI:4589877
 VERSION AB001693.1
 KEYWORDS Mn-SOD; manganese superoxide dismutase.
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 REFERENCE
 AUTHORS Ishida,N., Katayama,Y., Sato,F., Hasegawa,T. and Mukoyama,H.
 TITLE 1 (sites)
 JOURNAL The cDNA sequences of equine antioxidative enzyme genes Cu/Zn-SOD
 MEDLINE U. Vet. Med. Sci. 61 (3), 291-294 (1993)
 PUBMED 99261591
 REFERENCE 2 (bases 1 to 954)
 AUTHORS Ishida,N.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-1997) Nobushige Ishida, JRA Equine Research
 Institute, Laboratory of Molecular and Cellular Biology, 321-4,
 Tokami-Cho, Utsunomiya, Tochigi 320-0856, Japan
 (E-mail: noishida@center.equinist.go.jp, Tel:81-28-647-0662,
 Fax:81-28-647-0686)
 FEATURES
 SOURCE Location/Qualifiers
 1..954
 /organism="Equus caballus"
 /mol_type="mRNA"
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 /db_xref="taxon:9796"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="adult"
 /note="domestic horse"
 1..954
 /gene="Mn-SOD"
 70..738
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 /protein_id="BA076922.1"
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 QIMOLHSHKHAAYNNINVTBEKYQKALAKDVTATQALPALKFGNGGHINHTIFW
 INLSPNGGSEPKKILDAIKDFGSPDFKFKLTIVSAGVQSGGWLGFNKDQGRLO
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 ACKK"
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.000119 Length: 954
 Score: 80.00 Matches: 13
 Percent Similarity: 78.57% Conservative: 9
 Best Local Similarity: 46.43% Mismatches: 6
 Query Match: 55.17% Indels: 0
 DB: 4 Gaps: 0
 US-09-987-190-2 (1-30) x AB001693 (1-954)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 DB 142 AAGCAAGGCTCCCGACATTGCAGTATGATTATGGCGCTCTGGAGCCCTCATCAACGCC 201
 QY 21 GlnIleAsngluile***TyrThr 28
 DB 202 CAGATCATGACAGTCACACACAGC 225
 CDS

RESULT 31
 LOCUS GSP312188
 DEFINITION Gordonia sp. K02 sodA gene, ORF1, ORF2 and ORF3 (partial).
 ACCESSION AJ312188
 VERSION AJ312188.1 GI:21104320
 KEYWORDS ATP-binding protein; Mn-superoxide dismutase; ORF1; ORF2; ORF3;
 sodA gene; transmembrane protein.
 SOURCE Gordonia sp. K02
 ORGANISM Gordonia sp. K02
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Gordoniaceae; Gordonia.
 REFERENCE
 AUTHORS Berkeaa,M.M.
 JOURNAL Thesis (2001) Department of Institut fuer Mikrobiologie,
 Westfaelische Wilhelms-Universitaet Muenster, Muenster, Germany
 REFERENCE
 AUTHORS Berkeaa,M.M., Priefert,H. and Steinhuechel,A.
 TITLE Identification and characterization of an extracellular
 Mn-superoxide dismutase encoding gene (sod) of Gordonia sp. strain
 K02: A radical scavenger enzyme produced during rubber degradation
 Unpublished
 3 (bases 1 to 4439)
 AUTHORS Berkeaa,M.M.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAY-2001) Berkeaa M.M., Institut fuer Mikrobiologie,
 Westfaelische Wilhelms-Universitaet, Corrensstrasse 3,
 48149-Muenster, D-48149, GERMANY
 FEATURES
 SOURCE Location/Qualifiers
 1..4439
 /organism="Gordonia sp. K02"
 /mol_type="genomic DNA"
 /strain="Kb2"
 /db_xref="taxon:160824"
 /country="Germany:Muenster"
 /note="rubber degrading bacterium"
 1..640
 /gene="soda"
 1..3
 /gene="soda"
 11..640
 /gene="soda"
 /function="radical scavenger enzyme"
 /codon_start=1
 /evidence=experimental
 /transl_table=11
 /product="Mn-superoxide dismutase"
 /protein_id="CAC85367.1"
 /db_xref="GI:21104321"
 /db_xref="GOA:O8L1L4"
 /db_xref="SPTREMBL:O8L1L4"
 /translation="MAEYETADLDYDVAALPEPHISGRIMELHSHKHAAYVKGANDTL
 EKLAAKRDSDITAGKVGYSLTSEPHGCHHNSIPKFNLSPNGGSEEGPLAAITE
 QEGGDFDKRAIFTAATTLQSGMAATLGITDGKLVTLQITDGSNGIPALIIIVYML
 DMWEHAEFLDYQNVKPDVYKAMNVVWADAGEGRGAKTQSGILIEBA"
 complement (725..1519)
 /function="hypothetical ABC transport system"
 /note="ORF1"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC85368.1"
 /db_xref="GI:21104322"
 /db_xref="GOA:O8KJR7"
 /db_xref="SPTREMBL:O8KJR7"
 /translation="YSHRSAYRLGRCRCMTKTVPLROYPGDSFYHRLMAGTKIVTL
 ILGIMTWLPSWPLAGWVAIVITALLAGLPLGAIPEPPMWFGLIGIGVAPNNSFA
 GILGALIVRAITLALVVAISIIIVITTPMADVPALAIRPLRRLPVENAWA
 TALCMRGPLILIEELAVLRAARLRPTAKGRDHSASEMGINDLITAASSALRRSAE
 MAEAITARGGTRLTAAHPARPGRSALALFVIVACTVAVVTLLI"
 complement (1516..3765)
 /function="hypothetical ABC transport system"

CDS

Pred. No.: 0.000149 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x AN222758 (1-812)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTleSerGly 20
Db 74 AAGTACACGGTGGCGCGCGCTACACTACAGCGCGCTCGAGCGCGCATCTCGGCG 133
QY 21 GlnIleasnGluIle***Tyr 27
Db 134 GAGATCATGAGACGCACTAC 154

RESULT 34
LOCUS AY211085 429 bp mRNA linear INV 24-FEB-2003
DEFINITION Farfantepenaeus aztecus cytosolic manganese superoxide dismutase
ACCESSION AY211085
VERSION AY211085.1 GI:28544137
KEYWORDS Farfantepenaeus aztecus (brown shrimp)
SOURCE Farfantepenaeus aztecus
ORGANISM Farfantepenaeus aztecus (brown shrimp); Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eukaryota; Metazoa; Arthropoda; Decapoda; Dendrobranchiata; Penaeoidea; Penaeidae; Farfantepenaeus.

REFERENCE 1 (bases 1 to 429)
AUTHORS Brouwer, M. and Brown-Peterson, N.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2003) Department of Coastal Sciences, Univ. Southern Mississippi, 703 East Beach Drive, Ocean Springs, MS 39564, USA

FEATURES
Source location/Qualifiers
1..429
/organism="Farfantepenaeus aztecus"
/mol_type="mRNA"
/db_xref="taxon:6690"
CDS
1..429
/note="antioxidant enzyme"
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/product="cytosolic manganese superoxide dismutase"
/protein_id="AA042752.1"
/db_xref="GI:28544138"
/translation="EKXIAELVGEVDQIKKNQANADAVAIRMAVYEGIVVQ AGVADGVSVQIACMPAHINAEIGEEGHAHLPKXDPALEPHISGLIMEIHHTK HHGYNINLAIATKLVFAEADNDVSNANMLIPAIKFGGCG"

ORIGIN
Alignment Scores:
Pred. No.: 0.000102 Length: 429
Score: 78.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 53.79% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x AY211085 (1-429)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrTleSerGly 21
Db 223 CATGCTTTCGCACGCTCAAGTATGATTCAAGCGCCTTGAACCTCACATCTCGGCTTG 282
QY 22 IleasnGluIle***TyrThr 28
Db 283 ATCATGAGATCCACACACACA 303

RESULT 35
LOCUS BX248360 349659 bp DNA linear BCT 06-NOV-2003

DEFINITION Corynebacterium diptheriae gravis NCTC13129, complete genome; segment 7/8.
ACCESSION BX248360 BX248353
VERSION BX248360.1 GI:38200856
KEYWORDS complete genome.
SOURCE Corynebacterium diptheriae
ORGANISM Corynebacterium diptheriae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1 (bases 1 to 349659)
AUTHORS Cerdeno-Tarraga, A.M., Efstathiou, A., Dover, L.G., Holden, M.T.G., Pallen, M., Bentley, S.D., Beesa, G.S., Churcher, C., James, K.D., De Zeyza, A., Chillingworth, T., Cronin, A., Dowd, L., Felwell, T., Hamlin, N., Holroyd, S., Jagsels, K., Moule, S., Quail, M.A., Rabinowitch, E., Rutherford, K., Thomson, N.R., Unwin, L., Whitehead, S. and Barrell, B.G. Parkhill, J.
TITLE The complete genome sequence and analysis of Corynebacterium diptheriae NCTC13129
JOURNAL Nucleic Acids Res. 31 (22), 6516-6523 (2003)
PUBMED 14602910
REFERENCE 2 (bases 1 to 349659)
AUTHORS Cerdeno-Tarraga, A.M.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2003) Cerdeno-Tarraga A.M., submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: anct@sanger.ac.uk

FEATURES
Source location/Qualifiers
1..349659
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/mol_type="genomic DNA"
/strain="NCTC13129"
/db_xref="taxon:1717"
/note="biotype gravis"
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/complement(117..248)
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/locus_tag="DIP2033"
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/locus_tag="DIP2034"
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/locus_tag="DIP2034"
/note="HMMProfam hit to PF00872, Transposase, Mutator family"

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misc_feature	1053 . 1127 /locus_tag="DIP2036" /note="Signal peptide predicted for DIP2036 by Signalp 2.0.0. HMM (Signal peptide probability 1.000) with cleavage site probability 0.568 between residues 25 and 26; signal-peptide site"
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misc_feature	2276 . 3394 /locus_tag="DIP2037" /note="HMMpfam hit to PF01546, Peptidase family M20/M25/M40" 3581 . 3796 /locus_tag="DIP2038" 3581 . 3796 /locus_tag="DIP2038" /note="Doubtful CDS. No strong consensus RBS upstream. No significant database matches" /codon_start=1 /transl_table=1 /product="Hypothetical protein" /protein_id="CAE50565.1" /db_xref="GI:38200860"
gene	/translation="MFWRIVSSACLPAREQFLYPKPAPQDGPRGNVVKQKLLIATNALPATNAPHLQTLRRPLHTPS" 3804 . 4094 /locus_tag="DIP2039" 3804 . 4094 /locus_tag="DIP2039"

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membrane protein ML1504 SMALL:Q9CBX0 (EMBL:AL583922) (430
aa) fasta scores: E(): 1.8e-10, 31.8% id in 349 aa, and to
Mycobacterium tuberculosis hypothetical 47.1 kDa protein
Kv1159 or MTC165.26 SMALL:O06557 (EMBL:D95584)
(431 aa) fasta scores: E(): 4.3e-10, 31.66% id in 360 aa"
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/transl_table=1
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LVALVIMFARKQLTAGGVYAIAMAGMALLERISDFEYGOINILIMLVAMDPEP
HRTGIGLGAIGKILTPAIFIVILLIQRRAWASAVYATVAGTAVAGVWPPADPW
TKIPFSSRVGTQNTNGASLRAVLVRLDAEQVMTAIIAVLVAGGEWRARNPAM
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SPHLFFHDFKDFVCSLVEVAGVAILIPIAGYISARTASTGSOEPVSL"
4094..5180
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HMM (Signal peptide probability 0.942) with cleavage site
probability 0.430 between residues 29 and 30;
signal-peptide site"
/order(4112)..4165,4280..4333,4370..4429,4439..4498,
4511..4570,4583..4651,4664..4723,4844..4903,4922..4990,
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/locus_tag="DIP2042"
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/Note="Similar to Mycobacterium tuberculosis hypothetical
42.3 kDa protein Rv0433 or MT0448 or MTC122G10.30
SMALL:Y433_MYCTU (SMALL:P96279) (376 aa) fasta scores:
E(): 3e-78, 53.44% id in 363 aa, and to Halobacterium sp
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scores: E(): 9.3e-27, 32.85% id in 350 aa"
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AX123311 600 bp DNA PAT 11-MAY-2001
LOCUS AX123311
DEFINITION Sequence 3227 from Patent EP1108790.
ACCESSION AX123311
VERSION AX123311.1 GI:114040799
KEYWORDS
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinomycetales;
Corynebacteriaceae; Corynebacterium.
REFERENCE
1 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.,
Novel polynucleotides
Patent: EP 1108790-A 3227 20-JUN-2001;
JOURNAL KYOWA HAKKO KOGYO CO., LTD. (JP)
LOCATION/Qualifiers
1. 600
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
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Pred. No.: 0.000236 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
Gaps: 0
DB: 6
US-09-987-190-2 (1-30) x AX123311 (1-600)
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Db 10 TACGAACCTCCAGAACCTGACATACGACGCTCTCGAGCCACATCGCGCTGAA 69
QY 22 TleAsnGluIle**TyrThr 28
Db 70 ATCATGGAGCTTACCACTCC 90
RESULT 37
BD165428 600 bp DNA linear PAT 17-JAN-2003
LOCUS BD165428
DEFINITION Novel polynucleotide.
ACCESSION BD165428.1 GI:27871240
VERSION JP 2002191370-A/3227.
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 600)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.,
Novel polynucleotide
Patent: JP 2002191370-A 3227 09-JUL-2002;
JOURNAL KYOWA HAKKO KOGYO CO LTD
OS Corynebacterium glutamicum
PN JP 2002191370-A/3227
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOH, MASATO IKEDA, AKIO
OZAKI
PI
PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC
C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12P7/40, C12P13/
PC 04, C12P13/08,
PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC
G01N33/566,
PC G01N33/569, G01N33/68, G01N37/00//C12P21/08, (C12N1/21, C12R1/15),
PC (C12N1/21, C12R1/13), (C12N1/21, C12R1/01), (C12P13/08, C12R1/15),

PC C12N15/00,
PC C12N5/00, C12N15/00
CC Novel polynucleotide
FH key Location/Qualifiers
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Pred. No.: 0.000236 Length: 600
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Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
Gaps: 0
DB: 6
US-09-987-190-2 (1-30) x BD165428 (1-600)
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Db 10 TACGAACCTCCAGAACCTGACATACGACGCTCTCGAGCCACATCGCGCTGAA 69
QY 22 TleAsnGluIle**TyrThr 28
Db 70 ATCATGGAGCTTACCACTCC 90
RESULT 38
RABMSD 606 bp mRNA linear MAM 11-FEB-1994
LOCUS RABMSD
DEFINITION Oryctolagus cuniculus manganese superoxide dismutase mRNA, partial
cds.
ACCESSION L28808
VERSION L28808.1 GI:454174
KEYWORDS manganese superoxide dismutase.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
1 (bases 1 to 606)
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
JOURNAL Unpublished (1994)
AUTHORS Jackson, R.M.
COMMENT Original source text: Oryctolagus cuniculus (strain NZ white) CDNA
to mRNA.
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KRDGSPDKFERLTAIVSVGGSGWLGFNKEQGHQLQIACANQDPLQSTTGIIPL
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Pred. No.: 0.000239 Length: 606
Score: 77.00 Matches: 13
Percent Similarity: 78.57% Conservative: 9
Best Local Similarity: 46.43% Mismatches: 6
Query Match: 53.10% Indels: 0
Gaps: 0
DB: 4

US-09-987-190-2 (1-30) x RABMSD (1-606)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 16 AAGCAGAGCTCCCGACCTGCGCTACGACTACGCGCTGAGAGCCCGACATCAACCG 75
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 76 CAGATCATGAGCTTCACCATCAGC 99

RESULT 39
 AB055218 960 bp DNA linear BCT 02-AUG-2001
 LOCUS Corynebacterium glutamicum gene for superoxide dismutase, complete
 DEFINITION
 cdb.
 AB055218
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Corynebacterium glutamicum
 Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacteriaceae; Corynebacterium.

REFERENCE
 AUTHORS
 1 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Hattori, M.,
 Shiba, T., Sakaki, Y., Yokoi, H. and Ozaki, A.
 TITLE
 JOURNAL
 SOD of Corynebacterium glutamicum ATCC 13032
 REFERENCE
 AUTHORS
 2 Published Only in Database (2001)
 2 (bases 1 to 960)
 Nakagawa, S.
 TITLE
 JOURNAL
 Direct Submission
 Submitted (01-FEB-2001) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.
 Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
 Tokyo 194-8533, Japan (E-mail: snakagawa@kyowa.co.jp,
 Tel:81-42-725-2555 (ex.2165), Fax:81-42-726-8330)
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 Query Match: 53.10% Indels: 0
 DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x AB055218 (1-960)

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 Db 163 TACGAAGCTCCAGAACTCGACATACGATACGAGCTCTCGAGCAGACATCGCCGTGAA 222
 QY 22 IleAsnGluIle***TyrThr 28
 Db 223 ATCATGAGCTTCACCATC 243

RESULT 40
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LOCUS AR338437 1143 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 1 from patent US 6569650.
 ACCESSION AR338437
 VERSION AR338437.1 GI:33725209
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unclassified.

REFERENCE
 AUTHORS
 1 (bases 1 to 1143)
 Merkamm, M., Guyonvarch, A. and Marx, A.
 TITLE
 JOURNAL
 Patent: US 6569650-A 1 27-MAY-2003;
 FEATURES
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 Location/Qualifiers
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ORIGIN
 Alignment Scores:
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 Score: 77.00 Matches: 13
 Percent Similarity: 74.07% Conservative: 7
 Best Local Similarity: 48.15% Mismatches: 7
 Query Match: 53.10% Indels: 0
 DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x AR338437 (1-1143)

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 Db 347 TACGAAGCTCCAGAACTCGACATACGATACGAGCTCTCGAGCAGACATCGCCGTGAA 406
 QY 22 IleAsnGluIle***TyrThr 28
 Db 407 ATCATGAGCTTCACCATC 427

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 Job time : 6735 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 12:11:23 ; Search time 69 Seconds

(without alignments)
241.283 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145

Sequence: 1 KYSLEPDEFSATEPYISQINIXYTX 30

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
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Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%

Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	71.0	621	4	US-09-214-909-23
2	94	64.8	4403765	3	US-09-103-840A-2
3	94	64.8	4411529	3	US-09-103-840A-1
4	94	54.5	812	4	US-09-091-097-7
5	77	53.1	1143	4	US-09-373-731-1
6	74	51.0	594	3	US-09-075-019-1
7	74	51.0	600	6	5240847-8
8	74	51.0	600	6	5240847-9
9	74	51.0	600	6	5240847-16
10	74	51.0	600	6	5240847-17
11	74	51.0	681	3	US-09-075-019-6
12	74	51.0	813	2	US-08-927-230A-1

13	74	51.0	813	3	US-09-151-052-1
14	74	51.0	829	4	US-09-023-655-1348
15	74	51.0	969	2	US-08-365-486A-27
16	74	51.0	969	3	US-08-880-342-27
17	74	51.0	976	3	US-09-126-109-1
18	74	51.0	977	2	US-08-023-980B-2
19	74	51.0	977	2	US-08-486-953A-2
20	74	51.0	987	6	5240847-19
21	74	51.0	1032	6	5240847-25
22	74	51.0	3783	3	US-09-075-019-8
23	74	49.0	721	4	US-09-262-856A-8
24	70	48.3	1230025	4	US-09-198-452A-1
25	67	46.2	99	6	5240847-7
26	67	46.2	1830121	4	US-09-557-884-1
27	67	46.2	1830121	4	US-09-643-990A-1
28	63	43.4	375	4	US-09-488-039A-5014
29	63	43.4	654	4	US-09-489-039A-5056
30	63	43.4	702	4	US-09-489-039A-4999
31	62	42.8	728	4	US-09-091-097-5
32	58	40.0	675	4	US-09-543-681A-2482
33	58	40.0	719	3	US-09-411-578-39
34	58	40.0	719	4	US-09-749-233-39
35	58	40.0	726	4	US-09-540-236-1522
36	58	40.0	62909	4	US-09-596-002-32
37	57	39.3	606	4	US-09-134-001C-747
38	56	38.6	640681	4	US-09-790-988-1
39	55	37.9	618	4	US-09-543-681A-284
40	54	37.2	738	4	US-09-252-991A-7762
41	54	37.2	1145	4	US-08-956-171E-777
42	54	37.2	1176	4	US-09-252-991A-7571
43	54	37.2	3393	4	US-08-956-171E-426
44	53	36.6	780	1	US-08-445-909A-28
45	53	36.6	1294	1	US-08-445-909A-16

ALIGNMENTS

RESULT 1
US-09-214-909-23
Sequence 23, Application US/09214909
Patent No. 6486382
GENERAL INFORMATION:
APPLICANT: GORDON-KAMM, WILLIAM
APPLICANT: PIERCE, DOROTHY A.
APPLICANT: BOWEN, BENJAMIN
APPLICANT: BRIDNEY, DENNIS
APPLICANT: ROSS, MARGIT
APPLICANT: SCIELONGE, CHRISTOPHER
APPLICANT: MILLER, MICHAEL D.
APPLICANT: SANDAHL, GARY
APPLICANT: WANG, LITUN
TITLE OF INVENTION: USE OF THE GREEN FLUORESCENT PROTEIN AS A SCREENABLE
FILE REFERENCE: 031229/0682
CURRENT APPLICATION NUMBER: US/09/214,909
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US97/07688
PRIORITY FILING DATE: 1997-05-01
PRIORITY APPLICATION NUMBER: 60/016,345
PRIORITY FILING DATE: 1996-05-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 621
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(621)
OTHER INFORMATION: Description of Artificial Sequence: Superoxide
OTHER INFORMATION: Dismutase coding sequence fused to GFPm
US-09-214-909-23

```
Alignment Scores:
Pred. No.: 3,636-10 Length: 621
Score: 103.00 Matches: 17
Percent Similarity: 92.86% Conservative: 9
Best Local Similarity: 60.71% Mismatches: 2
Query Match: 71.03% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-214-909-23 (1-621)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 7 GAATACACGCTGGCGATCTGGATTAAGACTACAGCGCCCTGGAACCCACATCTCGGG 66
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 67 CAGATCAGCAGCTGCACCATTC 90

RESULT 2
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 0.00192 Length: 4403765
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-103-840A-2 (1-4403765)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4312963 GAATACACCTTGGCAGACTGAGCTAAGGAGCACTGGAAACCCACATCTCGG 4313022
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 4313023 CAGATCAGCAGCTGCACCATTC 4313046

RESULT 3
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
```

```
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 0.00193 Length: 4411529
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-103-840A-1 (1-4411529)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4320707 GAATACACCTTGGCAGACTGAGCTAAGGAGCACTGGAACCCACATCTCGG 4320766
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 4320767 CAGATCAGCAGCTGCACCATTC 4320790

RESULT 4
US-09-091-097-7
; Sequence 7, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812 base pairs
```

```

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..673
US-09-091-097-7

Alignment Scores:
Pred. No.: 1.62e-05 Length: 812
Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-091-097-7 (1-812)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 74 AAGTACACGCTCCGCGCTGCTACGACTACGCGCTCGAGCGCGGCGACTCTCGGCG 133
QY 21 GlnIleAsnGluIle**Tyr 27
Db 134 GAGATCATGAGGACGCACTAC 154

RESULT 5
US-09-373-731-1
; Sequence 1, Application US/09373731
; Patent No. 6569650
; GENERAL INFORMATION:
; APPLICANT: DEGUSSA-HULS AG
; APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
; TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
; TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
; FILE REFERENCE: MERKAM
; CURRENT APPLICATION NUMBER: US/09/373, 731
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Corynebacterium melassecola
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (338) ..(937)
US-09-373-731-1

Alignment Scores:
Pred. No.: 5.99e-05 Length: 1143
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-373-731-1 (1-1143)
QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
Db 347 TACGAACTCCGAACTCGACTACGACTACGAGCGCTCGAGCCACACATCGCGCTGAA 406
QY 22 IleAsnGluIle**TyrThr 28
Db 407 ATCATGAGCTTCACCACTCC 427

RESULT 6
US-09-075-019-1
; Sequence 1, Application US/09075019
; Patent No. 6130658
```

```

;
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Rosa P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..594
US-09-075-019-1

Alignment Scores:
Pred. No.: 9.28e-05 Length: 594
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-075-019-1 (1-594)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 1 AAGCAGACGCTCCCGACTGCGCTACGAGCGGCGCTGGAACCTCAGATCAACGCG 60
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 61 CAGATCATGAGCTGCACCAACG 84

RESULT 7
5240847-8
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 8
; LENGTH: 600
5240847-8
```

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-8 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCACACACTCT 87

RESULT 8
5240847-9
Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-POGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:9:
; LENGTH: 600

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-9 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCACACACTCT 87

RESULT 9
5240847-16
Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-POGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:16:
; LENGTH: 600

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10

Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-16 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCACACACTCT 87

RESULT 10
5240847-17
Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSER, EDELTRAUD; MAURER-POGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:17:
; LENGTH: 600

Alignment Scores:
Pred. No.: 9.41e-05 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x 5240847-17 (1-600)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTCTTGGCAGACTTGCACATACGACTAGCGTCTAGAACACACATCATGCT 63

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCATTCACACACTCT 87

RESULT 11
US-09-075-019-6
; Sequence 6, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:

```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 43..708
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 115..708
US-09-151-052-1

Alignment Scores:
Pred. No.: 0.00014 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-151-052-1 (1-813)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 115 AAGCAGAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGACCTCACAATCAAGCG 174

QY 21 GlnIleAsnGluLeu**TyrThr 28
Db 175 CAGATCATGCGAGCTGCACACAGC 198

RESULT 14
US-09-023-655-1348
Sequence 1348, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: g34710
US-09-023-655-1348

Alignment Scores:
Pred. No.: 0.000144 Length: 829
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-023-655-1348 (1-829)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 139 AAGCAGAGCCTCCCGACCTGCGCTACGACTACGCGCGCTGGACCTCACAATCAAGCG 198

QY 21 GlnIleAsnGluLeu**TyrThr 28
Db 199 CAGATCATGCGAGCTGCACACAGC 222

RESULT 15
US-08-365-486A-27
Sequence 27, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365.486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: human manganese superoxide dismutase
INDIVIDUAL ISOLATE: EMBL #X59445
FEATURE:
NAME/KEY: CDS
LOCATION: 61..729
US-08-365-486A-27

Alignment Scores:
Pred. No.: 0.000176 Length: 969
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10

Alignment Scores:

Pred. No.: 0.000178 Length: 976
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-126-109-1 (1-976)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 167 AAGCAGAGCCTCCCGGACCTGCGCTACGACTACGAGCGCGCTGGAACCTCAATCAACCGC 226

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 227 CAGATCATGCGAGCTGCACCAACGAC 250

RESULT 18

US-08-023-980B-2
Sequence 2, Application US/08023980B

Patent No. 5843641

GENERAL INFORMATION:

APPLICANT: Brown, Robert

APPLICANT: Horvitz, H. Robert

APPLICANT: Rosen, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,

TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP

STREET: 585 Commercial Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-1024

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/023,980B

FILING DATE: 26-FEB-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/177001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/723-4123

TELEFAX: 617/723-8962

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 977 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-023-980B-2

Alignment Scores:

Pred. No.: 0.000178 Length: 977
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0

US-09-987-190-2 (1-30) x US-08-023-980B-2 (1-977)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 168 AAGCAGAGCCTCCCGGACCTGCGCTACGACTACGAGCGCGCTGGAACCTCAATCAACCGC 227

QY 21 GlnIleAsnGluIle**TyrThr 28
Db 228 CAGATCATGCGAGCTGCACCAACGAC 251

RESULT 19

US-08-486-953A-2
Sequence 2, Application US/08486953A

Patent No. 5849290

GENERAL INFORMATION:

APPLICANT: Brown, Robert

APPLICANT: Horvitz, H. Robert

APPLICANT: Rosen, Daniel R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,

TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSeq

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,953A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/204,052

FILING DATE: 28-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/223002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/428-0200

TELEFAX: 617/428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 977 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-486-953A-2

Alignment Scores:

Pred. No.: 0.000178 Length: 977
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0

US-09-987-190-2 (1-30) x US-08-486-953A-2 (1-977)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 168 AAGCAGAGCCTCCCGGACCTGCGCTACGACTACGAGCGCGCTGGAACCTCAATCAACCGC 227

QY 21 GlnIleAsnGluIle**TyrThr 28

Db 228 CAGATCATGCGAGCTGCACCAACGAC 251

RESULT 20

5240847-19
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SEPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSZEK, EDELTRAUD; MAURER-FOGY, INGRID;
; MICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:19:
; LENGTH: 987
5240847-19
Alignment Scores:
Pred. No.: 0.00018 Length: 987
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x 5240847-19 (1-987)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 13 AAGACACTCTTGGCCAGACTGCGACATACGACTACGCTGTGAAGAACCATCATATGCT 72
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 73 CAATCATGCAATGACCACTCT 96
RESULT 21
5240847-25
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SEPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSZEK, EDELTRAUD; MAURER-FOGY, INGRID;
; MICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:25:
; LENGTH: 1032
5240847-25
Alignment Scores:
Pred. No.: 0.000191 Length: 1032
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x 5240847-25 (1-1032)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 73 AAGACAGCCCTCCCGACCTGCTACGACTACGCGCCCTGGAACCTCACATCAACGCG 132
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 133 CAGATCATGCACTGACCAACGAC 156
RESULT 22
US-09-075-019-8
; Sequence 8, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459

; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-075-019-8
Alignment Scores:
Pred. No.: 0.00105 Length: 3789
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x US-09-075-019-8 (1-3789)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 550 AAGACAGCCCTCCCGACCTGCTACGACTACGCGCCCTGGAACCTCACATCAACGCG 609
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 610 CAGATCATGCACTGACCAACGAC 633
RESULT 23
US-09-262-856A-8
; Sequence 8, Application US/09262856A
; Patent No. 633164
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutoh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikunoshi
; TITLE OF INVENTION: FUNERAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-372P
; CURRENT APPLICATION NUMBER: US/09/262,856A
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-262-856A-8

Alignment Scores:

Pred. No.:	0.000436	Length:	721
Score:	71.00	Matches:	13
Percent Similarity:	93.75%	Conservative:	2
Best Local Similarity:	81.25%	Mismatches:	1
Query Match:	48.97%	Indels:	0
DB:	4	Gaps:	0

US-09-987-190-2 (1-30) x US-09-262-856A-8 (1-721)

Qy 13 AlaThrGlnProTyrIleSerGlyGlnIleAsnGluLeu***TyrThr 28

Db 1 GCCACTGACCGTACATCACAGGAAATGACGAATTCATCTACT 48

RESULT 24

US-09-198-452A-1

Sequence 1, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(15000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

LOCATION: (15001)..(30000)

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

LOCATION: (420001)..(435000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

LOCATION: (435001)..(450000)

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NAME/KEY: misc_feature

LOCATION: (450001)..(465000)

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NAME/KEY: misc_feature

LOCATION: (465001)..(480000)

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LOCATION: (540001)..(555000)

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NAME/KEY: misc_feature

LOCATION: (555001)..(570000)

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NAME/KEY: misc_feature

LOCATION: (570001)..(585000)

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NAME/KEY: misc_feature

LOCATION: (585001)..(600000)

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NAME/KEY: misc_feature

LOCATION: (630001)..(645000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

LOCATION: (645001)..(660000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

LOCATION: (660001)..(675000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

LOCATION: (675001)..(690000)

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

LOCATION: (705001)..(720000)

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LOCATION: (735001)..(750000)

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NAME/KEY: misc_feature

LOCATION: (750001)..(765000)

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NAME/KEY: misc_feature

LOCATION: (765001)..(780000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

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NAME/KEY: misc_feature

LOCATION: (795001)..(810000)

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NAME/KEY: misc_feature

LOCATION: (810001)..(825000)

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NAME/KEY: misc_feature

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NAME/KEY: misc_feature

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LOCATION: (855001)..(870000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc_feature

LOCATION: (870001)..(885000)

OTHER INFORMATION: n=a or c or g or t

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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (690001)..(705000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (705001)..(720000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (720001)..(735000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (735001)..(750000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (750001)..(765000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (780001)..(795000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (795001)..(810000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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Alignment Scores:

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Pred. No.: 11.4 Length: 1230025
Score: 70.00 Matches: 13
Percent Similarity: 76.19% Conservative: 3
Best Local Similarity: 61.90% Mismatches: 5
Query Match: 48.28% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-198-452A-1 (1-1230025)

QY 2 TyrsleupProGluLeuAspTyGluPhsearlatrhguProTyrlsSerGly 21
Db 83327 TATTCTTACCGAGATTACCTATGATTAACCGCTTGAGCGCTGTAATTTCTTCGA 83386

QY 22 11e 22
Db 83387 ATT 83389

RESULT 25
5240847-7
Patent No. 5240847
APPLICANT: HECKL, KONRAD; SPEYAK, WALTER; OSTERMANN, ELINBORG;
ZOPHEL, ANDREAS; KRISTEK, EDELTRAUD; MAURER-FOGY, INGRID;
WITCHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
(HMN-SOD)
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/167,261
FILING DATE: 11-MAR-1988
SEQ ID NO: 7:
LENGTH: 99
5240847-7

Alignment Scores:
Pred. No.: 0.000182 Length: 99
Score: 67.00 Matches: 12
Percent Similarity: 76.00% Conservative: 7
Best Local Similarity: 48.00% Mismatches: 6
Query Match: 46.21% Indels: 0
DB: 6 Gaps: 0

US-09-987-190-2 (1-30) x 5240847-7 (1-99)

QY 1 TyrsleupProGluLeuAspTyGluPhsearlatrhguProTyrlsSerGly 20
Db 4 AAGCAGCTTTGCGAGCTTGCCATACGACTACGAGTCTCTAGAACCAACATCAATGCT 63

QY 21 11e 25
Db 64 CAAATCATGCAT 78

RESULT 26
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Alignment Scores:
Pred. No.: 69.7 Length: 1830121
Score: 67.00 Matches: 12
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 44.44% Mismatches: 9
Query Match: 46.21% Indels: 0
Gaps: 0
DB: 4

US-09-987-190-2 (1-30) x US-09-557-884-1 (1-1830121)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 1152886 TACACTCTCCCTGGAATTAGGCTATGACCTACATGCGTTAGAACCAATTGATGCGGCA 1152827
QY 22 IleAsnGluIle***TyrThr 28
Db 1152826 ACAATGGAATTCATCATAGT 1152806

RESULT 27
US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
```

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FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Alignment Scores:
Pred. No.: 69.7 Length: 1830121
Score: 67.00 Matches: 12
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 44.44% Mismatches: 9
Query Match: 46.21% Indels: 0
Gaps: 0
DB: 4

US-09-987-190-2 (1-30) x US-09-643-990A-1 (1-1830121)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 1152886 TACACTCTCCCTGGAATTAGGCTATGACCTACATGCGTTAGAACCAATTGATGCGGCA 1152827
QY 22 IleAsnGluIle***TyrThr 28
Db 1152826 ACAATGGAATTCATCATAGT 1152806

RESULT 28
US-09-489-039A-5014
Sequence 5014, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5014
LENGTH: 375
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5014

Alignment Scores:
Pred. No.: 0.00585 Length: 375
Score: 63.00 Matches: 12
Percent Similarity: 59.26% Conservative: 4
Best Local Similarity: 44.44% Mismatches: 11
Query Match: 43.45% Indels: 0
Gaps: 0
DB: 4

US-09-987-190-2 (1-30) x US-09-489-039A-5014 (1-375)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 293 TATACCTGCGCATCCCTGCTAGCATGCTGGAACCGCACTTGACAAGCAG 352
QY 22 IleAsnGluIle***TyrThr 28
Db 1152826 TACACTCTCCCTGGAATTAGGCTATGACCTACATGCGTTAGAACCAATTGATGCGGCA 1152827
```

Db 353 ACGATGAGATCATCACT 373

RESULT 29

US-09-489-039A-5056

Sequence 5056, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 5056

LENGTH: 654

TYPE: DNA

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-5056

Alignment Scores:

Pred. No.: 0.0121 Length: 654

Score: 63.00 Matches: 12

Percent Similarity: 59.26% Conservative: 4

Best Local Similarity: 44.44% Mismatches: 11

Query Match: 43.45% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-489-039A-5056 (1-654)

Qy 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyIn 21

Db 40 TATACCTGCGCATCCCTGCTTACGCTTACGATGCTCTGGAACCGCACTTGACACAGAG 99

Qy 22 IleAsnGluIle***TyrThr 28

Db 100 ACGATGAGATCATCACT 120

RESULT 30

US-09-489-039A-4999/c

Sequence 4999, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 4999

LENGTH: 702

TYPE: DNA

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-4999

Alignment Scores:

Pred. No.: 0.0133 Length: 702

Score: 63.00 Matches: 12

Percent Similarity: 59.26% Conservative: 4

Best Local Similarity: 44.44% Mismatches: 11

Query Match: 43.45% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-489-039A-4999 (1-702)

Qy 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyIn 21

Db 627 TATACCTGCGCATCCCTGCTTACGCTTACGATGCTCTGGAACCGCACTTGACACAGAG 568

Qy 22 IleAsnGluIle***TyrThr 28

Db 567 ACGATGAGATCATCACT 547

RESULT 31

US-09-091-097-5

Sequence 5, Application US/09091097

Patent No. 6432407

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH

APPLICANT: OKADO, TAKASHI

APPLICANT: YAGIHARA, TOMOKO

APPLICANT: KURODA, MASANOBU

APPLICANT: ONISHI, YOSHIMI

APPLICANT: KATO, IKUNOSHIN

APPLICANT: AKIYAMA, KAZUO

APPLICANT: YASUEDA, HIROSHI

APPLICANT: YAMAGUCHI, HIDEYO

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN

TITLE OF INVENTION: MALASSEZIA

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOIASCH & BIRCH, LLP

STREET: PO BOX 747

CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,097

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0346P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 728 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..618

US-09-091-097-5

Alignment Scores:

Pred. No.: 0.0215 Length: 728

Score: 62.00 Matches: 11

Percent Similarity: 66.67% Conservative: 7

Best Local Similarity: 40.74% Mismatches: 9

Query Match: 42.76% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-091-097-5 (1-728)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyIn 20

Db 16 GAGTACACTCTCCCTGCTTACGCTTACGATGCTCTGGAACCGCACTTGACACAGAG 75

Qy 21 GlnIleAsnGluIle***Tyr 27

Db 76 GAGATCATGACGGTCCACCAC 96

RESULT 32

US-09-543-681A-2482

Sequence 2482, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543.681A

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 2482

LENGTH: 675

TYPE: DNA

ORGANISM: Proteus mirabilis

US-09-543-681A-2482

Alignment Scores:

Pred. No.: 0.109 Length: 675

Score: 58.00 Matches: 11

Percent Similarity: 59.26% Conservative: 5

Best Local Similarity: 40.74% Mismatches: 11

Query Match: 40.00% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-543-681A-2482 (1-675)

Qy 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 58 TATACATTACCTGACATCCCTTATGATGCGCTAGAACCTCATTTGATGAGCGC 117

Qy 22 IleAsnGluIle***TyrThr 28

Db 118 ACATGGAAATTCACCATACT 138

RESULT 33

US-09-411-578-39

Sequence 39, Application US/09411578

Patent No. 6203801

GENERAL INFORMATION:

APPLICANT: Schaap, Theodorus C

APPLICANT: Kuiper, Catharina M

APPLICANT: Vermeulen, Arnoldus N

TITLE OF INVENTION: Coccioidosis Vaccines

FILE REFERENCE: schaap

CURRENT APPLICATION NUMBER: US/09/411,578

CURRENT FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: 98203384.7

EARLIER FILING DATE: 1998-10-07

EARLIER APPLICATION NUMBER: 98203457.1

EARLIER FILING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 39

LENGTH: 719

TYPE: DNA

ORGANISM: Eimeria tenella

US-09-411-578-39

Alignment Scores:

Pred. No.: 0.119 Length: 719

Score: 58.00 Matches: 12

Percent Similarity: 53.85% Conservative: 2

Best Local Similarity: 46.15% Mismatches: 12

Query Match: 40.00% Indels: 0

DB: 3 Gaps: 0

US-09-987-190-2 (1-30) x US-09-411-578-39 (1-719)

Qy 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 7 TTCGAACTCCCGCCGCGTACCCATGAGCGCTCGAGCCGTACATCAGCAAGAG 66

Qy 22 IleAsnGluIle***Tyr 27

Db 67 ACTCTCGAGTACCACTAT 84

RESULT 34

US-09-749-233-39

Sequence 39, Application US/09749233

Patent No. 6680061

GENERAL INFORMATION:

APPLICANT: Schaap, Theodorus C

APPLICANT: Kuiper, Catharina M

APPLICANT: Vermeulen, Arnoldus N

TITLE OF INVENTION: Coccioidosis Vaccines

FILE REFERENCE: schaap

CURRENT APPLICATION NUMBER: US/09/749,233

CURRENT FILING DATE: 2000-12-27

PRIOR FILING DATE: 1999-10-04

PRIOR APPLICATION NUMBER: 98203457.1

PRIOR FILING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 39

LENGTH: 719

TYPE: DNA

ORGANISM: Eimeria tenella

US-09-749-233-39

Alignment Scores:

Pred. No.: 0.119 Length: 719

Score: 58.00 Matches: 12

Percent Similarity: 53.85% Conservative: 2

Best Local Similarity: 46.15% Mismatches: 12

Query Match: 40.00% Indels: 0

DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-749-233-39 (1-719)

Qy 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 7 TTCGAACTCCCGCCGCGTACCCATGAGCGCTCGAGCCGTACATCAGCAAGAG 66

Qy 22 IleAsnGluIle***Tyr 27

Db 67 ACTCTCGAGTACCACTAT 84

RESULT 35

US-09-540-236-1522

Sequence 1522, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 1522

LENGTH: 726

TYPE: DNA

ORGANISM: M.catarrhalis

US-09-540-236-1522

Alignment Scores:

Pred. No.: 0.12 Length: 726

Score: 58.00 Matches: 10

Percent Similarity: 62.96% Conservative: 7

Job time : 1833 secs

/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.1002-001
/ CURRENT APPLICATION NUMBER: US/09/543,681A
/ CURRENT FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: US 60/128,706
/ PRIOR FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 8344
/ SEQ ID NO 284
/ LENGTH: 618
/ TYPE: DNA
/ ORGANISM: Proteus mirabilis
US-09-543-681A-284

Alignment Scores:
Pred. No.: 0.355 Length: 618
Score: 55.00 Matches: 11
Percent Similarity: 57.69% Conservative: 4
Best Local Similarity: 42.31% Mismatches: 11
Query Match: 37.93% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-543-681A-284 (1-618)

QY 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
:: |||||::|||
DB 46 TTCGAATTACCAAAATTACCTTAGCGTTGATGCTCTTGAGCCACACATCTCTAAAGAA 105

QY 22 IleAsnGluIle***Tyr 27
|||
DB 106 ACATTGAAATACCACTAC 123

RESULT 40

US-09-252-991A-7762
/ Sequence: 7762, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 7762
/ LENGTH: 738
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7762

Alignment Scores:
Pred. No.: 0.689 Length: 738
Score: 54.00 Matches: 11
Percent Similarity: 65.22% Conservative: 4
Best Local Similarity: 47.83% Mismatches: 8
Query Match: 37.24% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x US-09-252-991A-7762 (1-738)

QY 2 TyrsSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
:: |||||::|||
DB 163 TTCGAATTGCGCGCTGCTTAGCAAAAGACGCCCTTGAGCCGACATTTCGCGAGAA 222

QY 22 IleAsnGlu 24
|||
DB 223 ACCCTGGAA 231

Search completed: August 31, 2004, 22:27:54

PT comprises inducing mRNA expression of Mycobacterium tuberculosis and
PT detecting the induced mRNA.
XX
PS Example 5; Page 57-58; 70pp; English.
XX
CC The invention comprises a method for detecting the presence of a micro-
CC organism (particularly Mycobacterium tuberculosis) in a test sample. The
CC method of the invention comprises exposing the test sample to an inducer
CC that is capable of inducing the expression of at least one gene in the
CC micro-organism and then testing for the presence of mRNA from this gene.
CC The method of the invention is useful for detecting an mRNA that is
CC expressed in a species of Mycobacterium (e.g. Mycobacterium
CC tuberculosis). The present DNA sequence represents a Mycobacterium gene
CC which was used in an example of the invention. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 900 BP; 173 A; 297 C; 277 G; 153 T; 0 U; 0 Other;
DB:
Alignment Scores:
Pred. No.: 1,89e-08 Length: 900
Score: 101.00 Matches: 17
Percent Similarity: 92.86% Conservative: 9
Best Local Similarity: 60.71% Mismatches: 2
Query Match: 69.66% Indels: 0
Gaps: 0
DB:
US-09-987-190-2 (1-30) x ABT12955 (1-900)
QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSeryl 20
DB 266 GAATACACCCCTGCCGACCTGGACTGACGACTGAGCGGTAAGAACCGCACATCTCGGG 325
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 326 CAGATCAACGAGATCCACACAC 349
RESULT 2
ABT12954
ID ABT12954 standard; DNA; 1321 BP.
XX
AC ABT12954;
XX
DT 17-JAN-2003 (first entry)
XX
DE Mycobacterium tuberculosis soda gene sequence.
XX
KM Mycobacterium detection method; gene; ds; soda; scd; pncA.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200274991-A2.
XX
PD 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-GB001308.
XX
PR 20-MAR-2001; 2001GB-00006949.
XX
PI Karlsen F;
XX
DR WPI; 2002-750564/81.
XX
P-PSDB; AA015874.
XX
PA (NORC-) NORCHIP AS.
XX
PA (ALIA/) ALLARD S J.
XX
PT Detecting the presence of Mycobacterium tuberculosis in a test sample,
PT comprises inducing mRNA expression of Mycobacterium tuberculosis and
PT detecting the induced mRNA.
XX
PS Example 5; Page 55-56; 70pp; English.
XX
CC The invention comprises a method for detecting the presence of a micro-

CC organism (particularly Mycobacterium tuberculosis) in a test sample. The
CC method of the invention comprises exposing the test sample to an inducer
CC that is capable of inducing the expression of at least one gene in the
CC micro-organism and then testing for the presence of mRNA from this gene.
CC The method of the invention is useful for detecting an mRNA that is
CC expressed in a species of Mycobacterium (e.g. Mycobacterium
CC tuberculosis). The present DNA sequence represents a Mycobacterium gene
CC which was used in an example of the invention
XX
SQ Sequence 1321 BP; 266 A; 429 C; 382 G; 244 T; 0 U; 0 Other;
DB:
Alignment Scores:
Pred. No.: 5.81e-07 Length: 1321
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
Gaps: 0
DB:
US-09-987-190-2 (1-30) x ABT12954 (1-1321)
QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSeryl 20
DB 548 GAATACACCTTGCCGACCTGGACTGACGACTGAGCGGTAAGAACCGCACATCTCGGGT 607
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 608 CAGATCAACGAGATCCACACAC 631
RESULT 3
AA199683 43
Continuation (44 of 44) of AA199683 from base 4300001 (Mycobacterium tuberculosis strain
WP Sequence split into 44 fragments LOCUS AA199683 Accession AA199683
WP Fragment Name Begin End
WP AA199683_00 1 110000
WP AA199683_01 100001 210000
WP AA199683_02 200001 310000
WP AA199683_03 300001 410000
WP AA199683_04 400001 510000
WP AA199683_05 500001 610000
WP AA199683_06 600001 710000
WP AA199683_07 700001 810000
WP AA199683_08 800001 910000
WP AA199683_09 900001 1010000
WP AA199683_10 1000001 1110000
WP AA199683_11 1100001 1210000
WP AA199683_12 1200001 1310000
WP AA199683_13 1300001 1410000
WP AA199683_14 1400001 1510000
WP AA199683_15 1500001 1610000
WP AA199683_16 1600001 1710000
WP AA199683_17 1700001 1810000
WP AA199683_18 1800001 1910000
WP AA199683_19 1900001 2010000
WP AA199683_20 2000001 2110000
WP AA199683_21 2100001 2210000
WP AA199683_22 2200001 2310000
WP AA199683_23 2300001 2410000
WP AA199683_24 2400001 2510000
WP AA199683_25 2500001 2610000
WP AA199683_26 2600001 2710000
WP AA199683_27 2700001 2810000
WP AA199683_28 2800001 2910000
WP AA199683_29 2900001 3010000
WP AA199683_30 3000001 3110000
WP AA199683_31 3100001 3210000
WP AA199683_32 3200001 3310000
WP AA199683_33 3300001 3410000
WP AA199683_34 3400001 3510000
WP AA199683_35 3500001 3610000
WP AA199683_36 3600001 3710000
WP AA199683_37 3700001 3810000
WP AA199683_38 3800001 3910000

```
WP AA199683_39 3900001 4010000
WP AA199683_40 4000001 4110000
WP AA199683_41 4100001 4210000
WP AA199683_42 4200001 4310000
WP AA199683_43 4300001 4403765

Alignment Scores:
Pred. No.: 0.000161 Length: 103765
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x AA199683_43 (1-103765)

QY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 12963 GAATACACCTTGCCAGACTGGAGCTACGAGACACTGGAACCGACATCTCGGGT 13022
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 13023 CAGATCAACGAGCTTCACACAGC 13046

RESULT 4
AA199682_43
Continuation (44 of 45) of AA199682 from base 4300001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AA199682 Accession AA199682
WP Fragment Name Begin End
WP AA199682_00 1 110000
WP AA199682_01 100001 210000
WP AA199682_02 200001 310000
WP AA199682_03 300001 410000
WP AA199682_04 400001 510000
WP AA199682_05 500001 610000
WP AA199682_06 600001 710000
WP AA199682_07 700001 810000
WP AA199682_08 800001 910000
WP AA199682_09 900001 1010000
WP AA199682_10 1000001 1110000
WP AA199682_11 1100001 1210000
WP AA199682_12 1200001 1310000
WP AA199682_13 1300001 1410000
WP AA199682_14 1400001 1510000
WP AA199682_15 1500001 1610000
WP AA199682_16 1600001 1710000
WP AA199682_17 1700001 1810000
WP AA199682_18 1800001 1910000
WP AA199682_19 1900001 2010000
WP AA199682_20 2000001 2110000
WP AA199682_21 2100001 2210000
WP AA199682_22 2200001 2310000
WP AA199682_23 2300001 2410000
WP AA199682_24 2400001 2510000
WP AA199682_25 2500001 2610000
WP AA199682_26 2600001 2710000
WP AA199682_27 2700001 2810000
WP AA199682_28 2800001 2910000
WP AA199682_29 2900001 3010000
WP AA199682_30 3000001 3110000
WP AA199682_31 3100001 3210000
WP AA199682_32 3200001 3310000
WP AA199682_33 3300001 3410000
WP AA199682_34 3400001 3510000
WP AA199682_35 3500001 3610000
WP AA199682_36 3600001 3710000
WP AA199682_37 3700001 3810000
WP AA199682_38 3800001 3910000
WP AA199682_39 3900001 4010000
WP AA199682_40 4000001 4110000
WP AA199682_41 4100001 4210000
WP AA199682_42 4200001 4310000
WP AA199682_43 4300001 4410000
```

```
WP AA199682_44 4400001 4411529

Alignment Scores:
Pred. No.: 0.000174 Length: 110000
Score: 94.00 Matches: 15
Percent Similarity: 89.29% Conservative: 10
Best Local Similarity: 53.57% Mismatches: 3
Query Match: 64.83% Indels: 0
DB: 4 Gaps: 0

US-09-987-190-2 (1-30) x AA199682_43 (1-110000)

QY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 20707 GAATACACCTTGCCAGACTGGAGCTACGAGACACTGGAACCGACATCTCGGGT 20766
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 20767 CAGATCAACGAGCTTCACACAGC 20790

RESULT 5
AA199682_44
Continuation (44 of 45) of AA199682 from base 4400001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AA199682 Accession AA199682
WP Fragment Name Begin End
WP AA199682_00 1 110000
WP AA199682_01 100001 210000
WP AA199682_02 200001 310000
WP AA199682_03 300001 410000
WP AA199682_04 400001 510000
WP AA199682_05 500001 610000
WP AA199682_06 600001 710000
WP AA199682_07 700001 810000
WP AA199682_08 800001 910000
WP AA199682_09 900001 1010000
WP AA199682_10 1000001 1110000
WP AA199682_11 1100001 1210000
WP AA199682_12 1200001 1310000
WP AA199682_13 1300001 1410000
WP AA199682_14 1400001 1510000
WP AA199682_15 1500001 1610000
WP AA199682_16 1600001 1710000
WP AA199682_17 1700001 1810000
WP AA199682_18 1800001 1910000
WP AA199682_19 1900001 2010000
WP AA199682_20 2000001 2110000
WP AA199682_21 2100001 2210000
WP AA199682_22 2200001 2310000
WP AA199682_23 2300001 2410000
WP AA199682_24 2400001 2510000
WP AA199682_25 2500001 2610000
WP AA199682_26 2600001 2710000
WP AA199682_27 2700001 2810000
WP AA199682_28 2800001 2910000
WP AA199682_29 2900001 3010000
WP AA199682_30 3000001 3110000
WP AA199682_31 3100001 3210000
WP AA199682_32 3200001 3310000
WP AA199682_33 3300001 3410000
WP AA199682_34 3400001 3510000
WP AA199682_35 3500001 3610000
WP AA199682_36 3600001 3710000
WP AA199682_37 3700001 3810000
WP AA199682_38 3800001 3910000
WP AA199682_39 3900001 4010000
WP AA199682_40 4000001 4110000
WP AA199682_41 4100001 4210000
WP AA199682_42 4200001 4310000
WP AA199682_43 4300001 4410000

The present invention describes a method for monitoring differential
expression of genes in a first filamentous fungal (FF) cell relative to
expression of the same genes in one or more second filamentous fungal
cells. The method uses fluorescence-labeled nucleic acids isolated from
the FF cells and a substrate of expressed sequence tags (EST). The ESTs
are used in the method for monitoring differential expression of genes
in a first filamentous fungal (FF) cell relative to expression of genes
in one or more second filamentous fungal cells. Monitoring the
global expression of genes from FF cells allows the production potential
of the microorganisms to be improved. New genes may be discovered,
and possible functions of unknown open reading frames can be identified
and gene copy number variation and stability can be monitored. The expression
of genes can be used to study how FF cells adapt to changes in culture
conditions, environmental stress, spore morphogenesis, recombination,
```

metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AA07478 to AF11247 represents ESTs from *Psidium venenatum*; AF11248 to AF11853 represents ESTs from *Aspergillus niger*; AF11854 to AF14878 represents ESTs from *Aspergillus oryzae*; and AF14879 to AF15337 represents ESTs from *Trichoderma reesei*, which are all specifically claimed in the present invention.

Sequence 631 BP; 125 A; 223 C; 141 G; 134 T; 0 U; 8 Other;

Alignment Scores:

Pred. No.:	5.21e-05	Length:	631
Score:	81.00	Matches:	15
Percent Similarity:	75.00%	Conservative:	6
Best Local Similarity:	53.57%	Mismatches:	7
Query Match:	55.86%	Indels:	0
DB:	3	Gaps:	0

US-09-987-190-2 (1-30) x AA07909 (1-631)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 123 AAGGCCACTCTTCCGATCTTCCCTTACACACTAGCGGCGCTTGAGCCCTACATCTCGGC 182
21 GlnIleAsnGluIle**TyrThr 28
DB 183 CAGATCATGGAGCTCCACCACTCC 206

RESULT 6
AA05877
ID AA05877 standard; cDNA to mRNA; 812 BP.
AC AA05877;
DT 27-AUG-2003 (revised)
DT 23-FEB-1998 (first entry)
XX
DB Malassezia fungus MF-4 antigenic protein encoding cDNA.
XX
KM Malassezia; fungus; antigenic; human; IGE; immunoglobulin E; antibody;
KW allergy; antigen; ds.
XX
OS Malassezia.
XX
FH Key Location/Qualifiers
FH CDS 2..676
FT /*tag= a
FT /product= "MR-4_antigenic_protein"
XX
FN W09721817-A1.
XX
PD 19-JUN-1997.
XX
PF 10-DEC-1996; 96WO-JP003602.
XX
PR 12-DEC-1995; 95JP-00346627.
PR 05-SEP-1996; 96JP-00257612.
PR 05-SEP-1996; 96JP-00257613.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
PI Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI Akiyama K, Yasueda H, Yamaguchi H;
XX
DR WPI: 1997-332788/30.
DR P-PSDB; AAM29771.
XX
FT Antigenic proteins from the fungus *Malassezia* - bind to IGE antibodies
FT present in patients with *Malassezia* allergies, useful for diagnosis,
PT treatment and prevention of such conditions.

Claim 56; Page 77-78; 162pp; Japanese.

The present sequence encodes a specifically claimed antigenic protein isolated from the fungus *Malassezia*. The antigenic protein can bind to IGE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus *Malassezia* can be used in the diagnosis, treatment and prevention of allergic conditions due to *Malassezia* organisms (such as *M. furfur*, *M. sympodialis* and *M. pachydermatitis*). (Updated on 27-AUG-2003 to correct OS field.)

Sequence 812 BP; 235 A; 245 C; 218 G; 114 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.000167	Length:	812
Score:	79.00	Matches:	15
Percent Similarity:	70.37%	Conservative:	4
Best Local Similarity:	55.56%	Mismatches:	8
Query Match:	54.48%	Indels:	0
DB:	2	Gaps:	0

US-09-987-190-2 (1-30) x AA05877 (1-812)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 74 AAGTACAGCGTCCGCGCGCTCGCTACGACTACGCGGCGCTCGAGCCGATCTCGGC 133
21 GlnIleAsnGluIle**Tyr 27
DB 134 GAGATCATGGAGCGACACTAC 154

RESULT 7
AA06192
ID AA06192 standard; DNA; 600 BP.
AC AA06192;
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 3227.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
FN EPI108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOWA) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI: 2001-376931/40.
DR P-PSDB; AAG92973.
XX
FT Novel polynucleotides derived from *Coryneform* bacteria, for identifying
FT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 3227; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the *Coryneform* bacterium *Corynebacterium glutamicum*. These
CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 600 BP; 143 A; 197 C; 146 G; 114 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000261 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAH68192 (1-600)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 10 TACCAACTCCGAGACTGACTGACGATGACGCGCTCTCGAGCCACATGCGCGTGAA 69
QY 22 IleAsnGluIle**TyrThr 28
Db 70 ATCATGGAGGCTTCACCACTCC 90
RESULT 8
AAH68520
ID AAH68520 standard; DNA; 1143 BP.
XX
AC AAH68520;
XX
DT 09-MAY-2001 (first entry)
XX
DE C. melassecola superoxide dismutase DNA.
XX
KM Superoxide dismutase; sod; coryneform microorganism; metabolite; ds;
XX vitamin; D-pantothenic acid; L-lysine; amplification; animal nutrition.
XX
OS Corynebacterium melassecola.
XX
XX Key Location/Qualifiers
FH 338.940
FT CDS /*tag= a
FT /product= "Superoxide dismutase"
XX
XX EPI077261-A2.
XX
XX 21-FEB-2001.
XX
XX 02-AUG-2000; 2000EP-00116669.
XX
XX 13-AUG-1999; 99US-00373731.
XX
XX (DEGS) DEGUSSA-HUELS AG.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Merkmam M, Guyonvarch A, Marx A;
XX
XX WPI; 2001-212718/22.
XX
XX P-PSDB; AAU00514.
XX
XX New DNA encoding superoxide dismutase of Corynebacterium, useful for
XX producing transformants with increased production of metabolites,
XX particularly lysine.
XX
XX Claim 1; Page 13-14; 19pp; English.
XX
XX The sequence represents Corynebacterium melassecola superoxide dismutase
CC

CC (sod) DNA. Coryneform microorganisms may be transformed with a sod DNA
CC sequence and the sod gene can be amplified. Sod is then often
CC overexpressed in coryneform bacteria. Coryneforms that overexpress sod
CC are used for production of metabolites, particularly nucleotides,
CC vitamins and amino acids, especially D-pantothenic acid or, specifically,
CC L-lysine. These metabolites are useful in human or animal nutrition and
CC as pharmaceuticals. Overexpression of sod in coryneforms increases the
CC yield of particular metabolites
XX
SQ Sequence 1143 BP; 273 A; 323 C; 288 G; 259 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000598 Length: 1143
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: Gaps: 0
US-09-987-190-2 (1-30) x AAH68520 (1-1143)
QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 347 TACCAACTCCGAGACTGACTGACGATGACGCGCTCTCGAGCCACATGCGCGTGAA 406
QY 22 IleAsnGluIle**TyrThr 28
Db 407 ATCATGGAGGCTTCACCACTCC 427
RESULT 9
AAH68534
ID AAH68534 standard; DNA; 309400 BP.
XX
AC AAH68534;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7069.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
XX EPI108790-A2.
XX
XX 20-JUN-2001.
XX
XX 18-DEC-2000; 2000EP-00127688.
XX
XX 16-DEC-1999; 99JP-00377484.
XX 07-APR-2000; 2000JP-00159162.
XX 03-AUG-2000; 2000JP-00280988.
XX
XX (XYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tareishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analyzing
XX expression profile or pattern of a gene and identifying homologous gene.
XX
XX Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and analysing
XX the expression profile or expression pattern of a gene derived from
XX Coryneform bacterium, and identifying a homologue of a gene derived from
CC

CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office

XX Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.817	Length:	309400
Score:	77.00	Matches:	13
Percent Similarity:	74.07%	Conservative:	7
Best Local Similarity:	48.15%	Mismatches:	7
Query Match:	53.10%	Indels:	0
DB:	5	Gaps:	0

US-09-987-190-2 (1-30) x AAH68534 (1-309400)

OY 2 TyrsleupProgluleuAspTyrgluPheserAlathrgluProTyrlleserGlyln 21

Db 126401 TACCACTCCCGAAGCTGACATGACATGACACGCTCTCGAGCCACATCGCCGCTGAA 126460

OY 22 llsangluile**TyrrThr 28

Db 126461 ATCATGAGCTTCACCACTCC 126481

RESULT 10

AAQ94270 ID AAQ94270 standard; cDNA; 97 BP.

XX AC AAQ94270;

DT 25-MAR-2003 (revised)

DT 24-MAY-1996 (first entry)

XX Human Mn-superoxide dismutase (Lys29) N-terminal coding sequence.

XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;

KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;

XX osteoarthritis; wound healing; ds.

XX Synthetic.

XX Key location/Qualifiers

FT mat_peptide 4..97

FT /*tag= a

FT /note= "only encodes partial mature protein sequence,

FT i.e. N-terminal amino acids 1-31"

XX EPE6472-A1.

XX 11-OCT-1995.

XX 10-MAR-1998; 95EP-00107460.

XX 14-MAR-1987; 87DE-03708306.

XX 26-MAY-1987; 87DE-03717695.

XX 10-JUL-1987; 87DE-03722884.

XX 24-DEC-1987; 87DE-0374403B.

XX (BOEH) BOEHRINGER INGBLHEIM INT GMBH.

XX Heckl K, Spevak W, Ostermann E, Krystek E,

XX Maurel-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R,

XX WPI; 1995-346092/45.

XX Genes encoding recombinant human manganese superoxide dismutase - for

XX treatment, prevention and diagnosis of inflammatory diseases.

XX Claim 8; Page 5; 54pp; German.

CC A human placental cDNA library was screened with a probe derived from
CC which encoded sequences of human liver MnSOD. Two sequences were isolated
CC which encoded the majority (either amino acids 22-198 or 26-198) of
CC hMnSOD. To complete the 5'-ends of the cDNA sequences, a double-stranded
CC fragment (AAQ94270) coding for an initial Met residue followed by amino
CC acids 1-31 was synthesized using yeast preferred codons. Recombinant,
CC full-length hMn-SOD is useful for treating, preventing or diagnosing
CC inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
CC healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
CC field.)

XX Sequence 97 BP; 30 A; 30 C; 15 G; 22 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.76e-05	Length:	97
Score:	74.00	Matches:	12
Percent Similarity:	78.57%	Conservative:	10
Best Local Similarity:	42.86%	Mismatches:	6
Query Match:	51.03%	Indels:	0
DB:	2	Gaps:	0

US-09-987-190-2 (1-30) x AAQ94270 (1-97)

OY 1 LysTyrsleupProgluleuAspTyrgluPheserAlathrgluProTyrlleserGly 20

Db 4 AAGACCTCTTGGCAGACTGCGCATGACATGACGCTGCTGAGAACACACATCATGCT 63

OY 21 Glnllsangluile**TyrrThr 28

Db 64 CAANTCATGCAATTGACCACTCT 87

RESULT 11

ABX40730 ID ABX40730 standard; cDNA; 224 BP.

XX AC ABX40730;

DT 20-FEB-2003 (first entry)

XX Bovine BSR associated with lactation/muscle/fat deposition #5895.

XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;

KW muscle deposition; fat deposition; genome mapping; gene identification;

XX gene analysis; cattle breeding.

XX Bos Taurus.

XX US2002137139-A1.

XX 26-SEP-2002.

XX 24-SEP-2001; 2001US-00960352.

XX 12-JAN-1999; 99US-0115707P.

XX 11-JAN-2000; 2000US-00480902.

XX (BYAT/) BYATT J C.

XX (MATH/) MATHIALAGAN N.

XX (TAON/) TAO N.

XX (WARR/) WARREN W C.

XX Byatt JC, Mathialagan N, Tao N, Warren WC;

XX WPI; 2003-110599/10.

XX New nucleic acid associated with lactation, and muscle and fat

XX deposition, useful for genome mapping, gene identification and analysis,

XX cattle breeding, or for genetically improving cattle.

XX Claim 2; SEQ ID NO 5895; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with

XX lactation or muscle and fat deposition (designated LMFD), derived from

CC cattle, and the LMPD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX SQ Sequence 224 BP; 39 A; 83 C; 74 G; 28 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000258 Length: 224
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x ABX40730 (1-224)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 140 AAGCAGACGCTCCCGACCTGCGTACGACTACGAGCGCCCTGAGCGCCACATCAACGCG 199

QY 21 GlnIleAsnGluIle***TyrThr 28

DB 200 CAGATCATGACGCTGCACACACAGC 223

RESULT 12

ABX37856
ID ABX37856 standard; cDNA; 259 BP.

XX AC ABX37856;

XX AC 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #3021.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMPD;

XX KM muscle deposition; fat deposition; genome mapping; gene identification;

XX KM gene analysis; cattle breeding.

XX OS Bos Taurus.

XX XX US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat

XX deposition, useful for genome mapping, gene identification and analysis,

XX cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 3021; 245bp; English.

CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMPD), derived from
CC cattle, and the LMPD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX SQ Sequence 259 BP; 51 A; 96 C; 82 G; 30 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000311 Length: 259
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0

US-09-987-190-2 (1-30) x ABX37856 (1-259)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 142 AAGCAGACGCTCCCGACCTGCGTACGACTACGAGCGCCCTGAGCGCCACATCAACGCG 201

QY 21 GlnIleAsnGluIle***TyrThr 28

DB 202 CAGATCATGACGCTGCACACACAGC 225

RESULT 13

ABT33645
ID ABT33645 standard; DNA; 270 BP.

XX AC ABT33645;

XX AC 22-MAY-2003 (first entry)

XX DE Anticancer agent target gene fragment SEQ ID No 49.

XX KW DNA array; tumour; anticancer agent; drug tolerance factor; gene repair;

XX KM nucleic acid metabolism; large-scale gene-expression profiling;

XX KM housekeeping gene; ds.

```
OS Unidentified.
XX
XX WO2003004640-A1.
XX
XX 16-JAN-2003.
XX
XX 03-JUL-2002; 2002WO-JP006754.
XX
XX 05-JUL-2001; 2001JP-00204448.
XX
XX 07-AUG-2001; 2001JP-00239181.
XX
XX (TAIH ) TAIHO PHARM CO LTD.
XX
XX Takechi T, Koizumi K, Azuma A, Fukushima M;
XX
XX WPI; 2003-210360/20.
XX
XX DNA array for measuring expression of a number of different target gene
XX
XX fragments for measuring sensitivity of tumors to anticancer agents.
XX
XX Disclosure; Page 73; 83pp; Japanese.
XX
XX The invention relates to a novel DNA array for measuring sensitivity of a
XX
XX tumour to an anticancer agent comprising at least thirteen different
XX
XX target gene fragments selected from at least two types of gene including
XX
XX genes for, enzymes associated with nucleic acid metabolism, gene repair,
XX
XX factors associated with drug tolerance, and housekeeping genes. The array
XX
XX is used for large-scale gene-expression profiling, especially for
XX
XX assaying the sensitivity of tumours to anti-cancer agents. This
XX
XX polynucleotide sequence represents a target gene fragment of the
XX
XX invention
XX
XX Sequence 270 BP; 72 A; 86 C; 66 G; 46 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX
XX Pred. No.: 0.000328 Length: 270
XX
XX Score: 74.00 Matches: 12
XX
XX Percent Similarity: 78.57% Conservative: 10
XX
XX Best Local Similarity: 42.86% Mismatches: 6
XX
XX Query Match: 51.03% Indels: 0
XX
XX DB: Gaps: 0
XX
XX US-09-987-190-2 (1-30) x ABR33645 (1-270)
XX
XX QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
XX
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX 18 AAGGACAGCCTCCCGGACCTGCCCTACGACTAGCGCGCTCGAACCCTCATCATCAACGCG 77
XX
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 21 GlnIleAsnGluIle**TyrThr 28
XX
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX 78 CAGATCATGCAGCTGCACACACAGC 101
XX
XX
XX RESULT 14
XX
XX AAD39690
XX
XX ID AAD39690 standard; DNA; 325 BP.
XX
XX AC AAD39690;
XX
XX XX
XX
XX DT 22-OCT-2002 (first entry)
XX
XX XX
XX
XX DE Human MnSOD DNA.
XX
XX XX
XX
XX KM Antisense; human; antioxidant enzyme; manganese superoxide dismutase;
XX
XX MnSOD; catalase; glutathione peroxidase; neurodegenerative disease; CAT;
XX
XX GPx; heart disease; arthritis; tumour; therapy; gene; ds.
XX
XX XX
XX
XX OS Homo sapiens.
XX
XX XX
XX
XX Key Location/Qualifiers
XX
XX FT misc_feature 24..43
XX
XX FT /tag= a
XX
XX FT /note= "MnSOD antisense oligo 3"
XX
XX FT misc_feature 33..52
```

```
FT FT /tag= b
FT FT /note= "MnSOD antisense oligo 1"
FT FT CDS 41..325
FT FT /tag= d
FT FT /product= "Human MnSOD protein"
FT FT /transl_except= (pos:302..304, aa:Leu)
FT FT /note= "CDS does not include stop codon"
FT FT /partial
FT FT sig_peptide 41..112
FT FT /tag= e
FT FT misc_feature 41..59
FT FT /tag= c
FT FT /note= "MnSOD antisense oligo 2"
FT FT mat_peptide 113..325
FT FT /tag= f
FT FT /note= "Mature human MnSOD protein"
XX
XX WO200240498-A2.
XX
XX PN
XX
XX XX
XX
XX PD 23-MAY-2002.
XX
XX XX
XX
XX PF 14-NOV-2001; 2001WO-US044241.
XX
XX XX
XX
XX PR 14-NOV-2000; 2000US-0248328P.
XX
XX XX
XX
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX
XX PI Oberley LW, Weydert CT, Smith BB;
XX
XX XX
XX
XX DR WPI; 2002-500199/53.
XX
XX DR P-PSDB; AAE24641.
XX
XX XX
XX
XX PT New oligonucleotides, useful for treating antioxidant enzyme malfunction
XX
XX disorder, comprises antisense nucleic acid sequence that specifically
XX
XX binds to antioxidant enzyme start codon.
XX
XX XX
XX
XX PS Disclosure; Fig 1; 36pp; English.
XX
XX XX
XX
XX CC The invention relates to an antisense oligonucleotide that specifically
XX
XX bind to an antioxidant enzyme start codon. Antioxidant enzymes of the
XX
XX CC invention include manganese superoxide dismutase (MnSOD), catalase (CAT)
XX
XX CC and glutathione peroxidase (GPx) etc. Antisense compounds of the
XX
XX CC invention are useful for treating antioxidant enzyme malfunction
XX
XX CC disorders such as heart disease, arthritis, neurodegenerative disease,
XX
XX CC and tumour. They are also used in antisense therapy. The present sequence
XX
XX is human MnSOD DNA
XX
XX XX
XX
XX SQ Sequence 325 BP; 76 A; 99 C; 98 G; 52 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX
XX Pred. No.: 0.000416 Length: 325
XX
XX Score: 74.00 Matches: 12
XX
XX Percent Similarity: 78.57% Conservative: 10
XX
XX Best Local Similarity: 42.86% Mismatches: 6
XX
XX Query Match: 51.03% Indels: 0
XX
XX DB: Gaps: 0
XX
XX US-09-987-190-2 (1-30) x AAD39690 (1-325)
XX
XX QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
XX
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX DB 113 AAGGACAGCCTCCCGGACCTGCCCTACGACTAGCGCGCTCGAACCCTCATCATCAACGCG 172
XX
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX QY 21 GlnIleAsnGluIle**TyrThr 28
XX
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX
XX DB 173 CAGATCATGCAGCTGCACACACAGC 196
XX
XX
XX RESULT 15
XX
XX AAC02178
XX
XX ID AAC02178 standard; cDNA; 414 BP.
XX
XX XX
XX
XX AC AAC02178;
XX
XX XX
```

DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 2176.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EPI033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
DR P-PSDB; AAG02172.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 2176; 71np + Sequence listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC cDNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 414 BP; 89 A; 124 C; 126 G; 73 T; 0 U; 2 Other;
XX
Alignment Scores:
Pred. No.: 0.000568 Length: 414
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AAC02178 (1-414)
QY 1 LysTyrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 182 AAGCAGAGCCTCCCGACCTGACGACACGCGCCCTGGAACCTCACATCAACGCG 241
QY 21 GluIleAsnGluIle**TyrThr 28
DB 242 CAGATCATGCGAGCTGCGACACAGC 265
RESULT 16
ABX49579
ID ABX49579 standard; cDNA; 424 BP.
XX
AC ABX49579;
XX
DT 21-FEB-2003 (first entry)
XX

DE Bovine EST associated with lactation/muscle/fat deposition #14744.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137139-A1.
XX
PD 26-SEP-2002.
XX
PF 24-SEP-2001; 2001US-00960352.
XX
PR 12-JAN-1999; 99US-0115707P.
XX
PR 11-JAN-2000; 2000US-00480902.
XX
PA (BYAT/) BYATT J C.
XX
PA (MATH/) MATHIALAGAN N.
XX
PA (TAON/) TAO N.
XX
PA (WAR/) WARREN W C.
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX
DR WPI; 2003-110599/10.
XX
PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
PS Claim 2; SEQ ID NO 14744; 245bp; English.
XX
CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 424 BP; 95 A; 129 C; 135 G; 65 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000586 Length: 424
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x ABX49579 (1-424)
QY 1 LysTyrSerLeuProGluLeuAspTYrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 182 AAGCAGAGCCTCCCGACCTGACGACACGCGCCCTGGAACCTCACATCAACGCG 241
QY 21 GluIleAsnGluIle**TyrThr 28
DB 242 CAGATCATGCGAGCTGCGACACAGC 265
RESULT 16
ABX49579
ID ABX49579 standard; cDNA; 424 BP.
XX
AC ABX49579;
XX
DT 21-FEB-2003 (first entry)
XX

```

Db 121 AAGCAGACGCTCCCGACGCTGCGTACGACTACGCGCCCTGAGCGGCACATCAGCGC 180
QY 21 Glnlleasnngluile***TyrThr 28
Db 181 CAGATCATGCACTGACACACGACG 204
RESULT 17
AAZ08755
ID AAZ08755 standard; cDNA, 552 BP.
AC AAZ08755;
XX
XX 03-NOV-1999 (first entry)
XX
DE Human manganese superoxide dismutase exon 3-deleted isoform cDNA.
XX
XX Human; manganese superoxide dismutase; MnSOD; exon 3 deleted isoform;
KM MnSOD E3(-); diagnosis; viral infection; HIV; oncogenesis; tumour;
KW UV-induced damage; post ischaemia reperfusion damage; anti-inflammatory;
KW cytotoxic; cardiotoxic; cancer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1..552
XX FT /*tag= a
XX FT /product= "MnSOD E3(-)"
XX FT /note= "manganese superoxide dismutase exon 3-deleted
XX FT isoform"
XX
XX W09943697-A1.
XX
XX 02-SEP-1999.
XX
XX 25-FEB-1999; 99WO-US004129.
XX
XX 25-FEB-1998; 98US-0075948P.
XX
XX (UYCO-) UNIV & COMMUNITY COLLEGE.
XX
XX Anziano PQ;
XX
XX WPI; 1999-527592/44.
XX
XX P-PSDB; AAY29656.
XX
XX A new isoform useful for diagnosing oxidative stress, and treating viral
XX infections.
XX
XX Claim 2; Page 12; 64pp; English.
XX
XX The present sequence encodes an isoform of manganese superoxide dismutase
XX (MnSOD), which is a splice-variant lacking exon 3 of the full length
XX MnSOD (i.e. MnSOD E3(-)). MnSOD E3(-) may be useful in the treatment of a
XX wide variety of disorders including viral infections, particularly HIV,
XX and may be used for the prevention of oncogenesis, tumour promotion and
XX invasiveness, and UV-induced damage, for protection of cardiac tissue
XX against post ischaemia reperfusion damage, as an anti-inflammatory agent,
XX to reduce the cytotoxic and cardiotoxic effects of anti-cancer drugs, and
XX to improve the longevity of living cells
XX
XX Sequence 552 BP; 145 A; 135 C; 153 G; 119 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000823 Length: 552
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAZ08755 (1-552)

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QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 73 AAGCAGACGCTCCCGACGCTGCGTACGACTACGCGCCCTGGAACCTCAGATCAGCGC 132
QY 21 Glnlleasnngluile***TyrThr 28
Db 133 CAGATCATGCACTGACACACGACG 156
RESULT 18
AAQ73584
ID AAQ73584 standard; DNA, 561 BP.
AC AAQ73584;
XX
XX 25-MAR-2003 (revised)
XX
XX 25-JUN-1995 (first entry)
XX
DE Human manganese superoxide dismutase variant gene.
XX
XX MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX
XX Homo sapiens.
XX
XX W09421283-A1.
XX
XX 29-SEP-1994.
XX
XX 24-MAR-1994; 94WO-US003185.
XX
XX 24-MAR-1993; 93US-00036604.
XX
XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
XX Wegner C, Wolyniec KW;
XX
XX WPI; 1994-316659/39.
XX
XX Improved inhibition of pulmonary oxygen toxicity - by prophylactic,
XX topical admin. of human mitochondrial manganese superoxidisedismutase.
XX
XX Claim 7; Page 27; 41pp; English.
XX
XX The sequence is that of a mutant human manganese superoxide dismutase
XX tetramer. Mutations of the native protein provide a protein which, when
XX applied topically, can inhibit pulmonary oxygen toxicity. See also
XX AAQ73582-5. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 561 BP; 160 A; 126 C; 139 G; 136 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAQ73584 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTTTGGCAGACTTGCATACGACTACGCGGTGCTTGAACACACATCAATGCT 63
QY 21 Glnlleasnngluile***TyrThr 28
Db 64 CAATCATGCAATTCACCACTCT 87
RESULT 19
AAQ73582
ID AAQ73582 standard; DNA, 561 BP.
XX
XX AAQ73582;
XX

```

DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Human manganese superoxide dismutase gene.
XX
KM MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX
OS Homo sapiens.
XX
PN W09421283-A1.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US003185.
XX
PR 24-MAR-1993; 93US-00036604.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Wegner C, Wolynecic WW;
XX
DR WPI; 1994-31659/39.
XX
PT Improved inhibition of pulmonary oxygen toxicity - by propylactic,
PT topical admin. of human mitochondrial manganese superoxidisedismutase.
XX
PS Claim 6; Page 25; 41pp; English.
XX
CC The sequence is that of the native human manganese superoxide dismutase
CC tetramer. Mutations in this sequence, esp. CAG for AAG at codon 30 or CAT
CC for CAG at codon 32 provides a protein which, when applied topically, can
CC inhibit pulmonary oxygen toxicity. See also AAQ73583-5. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 561 BP; 160 A; 127 C; 139 G; 135 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAQ73582 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 4 AAGCACTCTTTGCCAGACTTGCCATACGACTACGCTGTCTTAAGAACCAACATCAATGCT 63
QY 21 GlnIleAsnGluIle**TyrThr 28
DB 64 CAATCATGCAATGCACCACTCT 87
RESULT 20
AAQ73585
ID AAQ73585 standard; DNA; 561 BP.
XX
AC AAQ73585;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Human manganese superoxide dismutase variant gene.
XX
KM MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX
OS Homo sapiens.
XX
PN W09421283-A1.
XX
PD 29-SEP-1994.

PF 24-MAR-1994; 94WO-US003185.
XX
PR 24-MAR-1993; 93US-00036604.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Wegner C, Wolynecic WW;
XX
DR WPI; 1994-31659/39.
XX
PT Improved inhibition of pulmonary oxygen toxicity - by propylactic,
PT topical admin. of human mitochondrial manganese superoxidisedismutase.
XX
PS Claim 7; Page 26; 41pp; English.
XX
CC The sequence is that of a mutant human manganese superoxide dismutase
CC tetramer. Mutations of the native protein provide a protein which, when
CC applied topically, can inhibit pulmonary oxygen toxicity. See also
CC AAQ73582-4. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 561 BP; 159 A; 127 C; 139 G; 136 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0
US-09-987-190-2 (1-30) x AAQ73585 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 4 AAGCACTCTTTGCCAGACTTGCCATACGACTACGCTGTCTTAAGAACCAACATCAATGCT 63
QY 21 GlnIleAsnGluIle**TyrThr 28
DB 64 CAATCATGCAATGCACCACTCT 87
RESULT 21
AAQ73583
ID AAQ73583 standard; DNA; 561 BP.
XX
AC AAQ73583;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Human manganese superoxide dismutase variant gene.
XX
KM MnSOD; tetramer; pulmonary oxygen toxicity; mitochondrial; mutant; ss.
XX
OS Homo sapiens.
XX
PN W09421283-A1.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US003185.
XX
PR 24-MAR-1993; 93US-00036604.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Wegner C, Wolynecic WW;
XX
DR WPI; 1994-31659/39.
XX
PT Improved inhibition of pulmonary oxygen toxicity - by propylactic,
PT topical admin. of human mitochondrial manganese superoxidisedismutase.
XX
PS Claim 7; Page 26; 41pp; English.

XX The sequence is that of a mutant human manganese superoxide dismutase
CC tetramer. Mutations of the native protein provide a protein which, when
CC applied topically, can inhibit pulmonary oxygen toxicity. See also
CC AA073582-5. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 561 BP; 159 A; 128 C; 139 G; 135 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000841 Length: 561
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
DB: 2
US-09-987-190-2 (1-30) x AA073583 (1-561)
QY 1 LysTyrSerLeuProGluLeuAspTyrGlnPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCAGCTCTTGGCAGACTTGCCATACGACTACGCTGCTCTAGAACACACATCATGCT 63
QY 21 GlnTleAsnGluIle***TyrThr 28
Db 64 CAATCATGCAATGCACCACTCT 87
RESULT 22
AAZ39779
ID AAZ39779 standard; cDNA; 594 BP.
XX
AC AAZ39779;
XX
DT 06-MAR-2000 (first entry)
XX
DE Human manganese superoxide dismutase (MnSOD) protein encoding cDNA.
XX
KM Manganese superoxide dismutase; MnSOD; ECSOD; proteoglycan; human;
KM endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
KM lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
KM hyperoxia; atherosclerosis; lupus erythematosus; hypertension;
KM neutrophil-mediated inflammation; ss.
XX
OS Homo sapiens.
XX
OS
XX
PN M0958547-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009921.
XX
PR 08-MAY-1998; 98US-00075019.
XX
PA (WEBB-) WEBB-WARING INST BIOMEDICAL RES.
XX
PI Mccord JM, Gao B, Flores SC;
XX
DR WPI; 2000-062283/05.
DR P-PSDB; AAY55846.
XX
PT Modified manganese superoxide dismutase, methods of production and
PT antibodies.
XX
PS
XX
XX Claim 6; Page 71-72; 83pp; English.
XX
XX The invention provides a nucleic acid molecule encoding a genetically
XX modified manganese superoxide dismutase (MnSOD). The nucleic acid
XX comprises: a first nucleic acid sequence encoding an enzymatically active
XX portion of MnSOD; and a second nucleic acid sequence encoding a peptide
XX (ECSOD) that binds to polyanionic polysaccharides or proteoglycans on
XX endothelial cell surfaces. The protein protects a mammal, especially
XX humans, from oxidative damage and especially from conditions consisting
XX of pulmonary inflammatory injury, lung disease, cancer, hypoxia, ischemia
XX reperfusion injury, hyperoxia, atherosclerosis, arthritis, hypoxia

CC erythematosus, hypertension and neutrophil-mediated inflammation. The
CC lung disease is infant or adult respiratory distress syndrome.
CC interstitial lung disease or asthma. The mutant MnSOD also protects
CC organs of mammals from pre- and post-transplantation oxidative damage.
CC MnSOD is positively charged at physiological pH and has a longer plasma
CC half-life of about 4 hours compared to 6-15 minutes for cytosolic Cu,Zn
CC SOD (following intravenous injection). ECSOD has a substantial advantage
CC over both Cu, ZnSOD and MnSOD because of its ability to bind to the
CC endothelium. ECSOD is hard to produce in mammalian cell culture systems,
CC so a fusion of ECSOD and MnSOD therefore overcomes these problems. The
CC present sequence represents a cDNA encoding a human MnSOD protein
SQ Sequence 594 BP; 166 A; 144 C; 154 G; 130 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000905 Length: 594
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
DB: 3
US-09-987-190-2 (1-30) x AAZ39779 (1-594)
QY 1 LysTyrSerLeuProGluLeuAspTyrGlnPheSerAlaThrGluProTyrIleSerGly 20
Db 1 AAGCAGAGCCTCCCGACCTGCGCTACGACTACGCGCGCCCTGGAACCTCATCATCAGCG 60
QY 21 GlnTleAsnGluIle***TyrThr 28
Db 61 CAGATCATGCAAGCTGCACACACAGC 84
RESULT 23
AAN81225
ID AAN81225 standard; cDNA; 600 BP.
XX
AC AAN81225;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-1990 (first entry)
XX
DE cDNA of formula VIIb encoding complete human manganese superoxide
DE dismutase (MnSOD).
XX
KM Human manganese superoxide dismutase derivative; clone B88; formula VIIb;
KM enzyme; BC-1.15.1.1.
XX
XX
XX Homo sapiens.
XX
OS
XX
PN EP282899-A.
XX
PD 21-SEP-1998.
XX
PF 10-MAR-1998; 88EP-00103754.
XX
PR 14-MAR-1987; 87DE-03708306.
PR 26-MAY-1987; 87DE-03717695.
PR 10-JUN-1987; 87DE-03722884.
PR 24-DEC-1987; 87DE-03744038.
XX
PA (BOEH) BOEHRINGER INGELHEIM.
XX
PI Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
PI Maurerfogel I, Wichnecasta MJ, Stralow C;
XX
DR WPI; 1988-265361/38.
XX
XX Prodn. of human manganese superoxidizedismutase peptide(s) - and DNA coding
XX sequences, for control and diagnosis of e.g. inflammatory diseases.
XX
PS Disclosure; Page 7; 57pp; German.
XX
XX The patent is for polypeptides, esp. non-glycosylated, having the

CC	enzymatic, biological and immunological properties of hmsOD that are
CC	prepared by genetic engineering methods. Also new are DNA sequences
CC	encoding all or part of the polypeptides and replicating vectors,
CC	expression plasmids and transformed host cells confy. these sequences.
CC	hmsOD catalyses disproportionation of the superoxide radical and can be
CC	used in the prevention, diagnosis and treatment of inflammatory,
CC	degenerative, neoplastic and rheumatoid disorders; for wound healing;
CC	autoimmune disease and in organ transplantation. It can also be used to
CC	improve the storage stability of liq. and solid foods. Oligo Via
CC	(XhoI/XbaI) (AAN81222) was ligated to oligo VIB (XbaI/NcoI) (AAN81223)
CC	and then used to produce cDNA encoding the entire hmsOD of formula VIIa
CC	(AAN81224) and formula VIIB . (Updated on 25-MAR-2003 to correct PR
CC	field.)
XX	
SQ	Sequence 600 BP, 172 A, 134 C, 150 G, 144 T, 0 U, 0 Other;
Alignment Scores:	
Pred. No.:	0.000917
Score:	74.00
Percent Similarity:	78.57%
Best Local Similarity:	42.86%
Query Match:	51.03%
DB:	1 Gaps: 0
US-09-987-190-2 (1-30) x AAN81225 (1-600)	
CY	1 LysTyrSerLeuProGluIleuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
Db	4 AAGCACTCTTGCCACACTTGCATTCGACCTACGGTGTCTTAGAACACACATCATCT 63
CY	21 GluIleShnGluIle**TyrThr 28
Db	64 CAATTCATCGAATTGCACACACTCT 87
RESULT 24	
AAN81218	
ID	AAN81218 standard; cDNA; 600 BP.
XX	
AC	AAN81218;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-1990 (first entry)
XX	
DE	Sequence of Formula IIA encoding modified portion of human manganese
DE	superoxide dismutase (hmsOD).
KW	Human manganese superoxide dismutase derivative; clone B58; formula IIIa
KW	enzyme; EC-1.15.1.1.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 4..600
XT	/**tag= a
PN	EP282899-A.
XX	
PD	21-SEP-1988.
XX	
PF	10-MAR-1988; 88BP-00103754.
XX	
PR	14-MAR-1987; 87DE-03708306.
PR	26-MAY-1987; 87DE-03717695.
PR	10-JUL-1987; 87DE-03722884.
PR	24-DEC-1987; 87DE-03744038.
XX	
EA	(BOEH) BOEHRINGER INGELHEIM.
PI	Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
PI	Mauterfogy I, Wichneasta MJ, Stralow C;
XX	WP1, 1988-265361/38.
OR	P-PSDB; AAP80602.

```

XX PT Prodn. of human manganese superoxide dismutase peptide(s) - and DNA coding
XX sequences, for control and diagnosis of e.g. inflammatory diseases.
XX
XX PS Disclosure, Page 7; 57pp; German.
XX
CC CC The patent is for polypeptides, esp. non-glycosylated, having the
CC enzymatic, biological and immunological properties of hmnSOD that are
CC prepd. by genetic engineering methods. Also new are DNA sequences
CC encoding all or part of the polypeptides and replicating vectors,
CC expression plasmids and transformed host cells contg. these sequences.
CC hmnSOD catalyses disproportionation of the superoxide radical and can be
CC used in the prevention, diagnosis and treatment of inflammatory,
CC degenerative, neoplastic and rheumatoid disorders; for wound healing, in
CC autoimmune disease and in organ transplantation. It can also be used to
CC improve the storage stability of liq. and solid foods. AAN81218 is
CC derived from Formula Ia (AAN81825). (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 600 BP; 173 A; 134 C; 150 G; 143 T; 0 U; 0 Other;
XX
XX Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 1 Gaps: 0
XX
US-09-987-190-2 (1-30) x AAN81218 (1-600)
XX
CY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 4 AAGCACTCTTTGCCGACTTGCCATACGACTACGGTCTCTAGAACACACATCATGCT 63
CY 21 GlnIleAsnGluIle**TyrThr 28
Db 64 CAATCATGCAATTGCACCACTCT 87
XX
RESULT 25
AAN81224
ID AAN81224 standard; cDNA; 600 BP.
XX
AC AAN81224;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-1990 (first entry)
XX
DE cDNA of formula VIIa encoding complete human manganese superoxide
DE dismutase (hmnSOD).
XX
KM Human manganese superoxide dismutase derivative; clone B58; formula VIIa;
KW enzyme; EC-1.15.1.1.
XX
XX Homo sapiens.
OS
XX EP282899-A.
XX
PD 21-SEP-1988.
XX
XX 10-MAR-1988; 88EP-00103754.
XX
XX 14-MAR-1987; 87DE-03708306.
XX 26-MAY-1987; 87DE-03717695.
XX 10-JUL-1987; 87DE-03722884.
XX 24-DEC-1987; 87DE-03744038.
XX
XX (BOEH ) BOEHRINGER INGELHEIM.
XX
PI Heckl K, Spevak W, Ostermann E, Zophel A, Kryatek E;
PI Maurerfogt I, Wichneasta MJ, Stralow C;
XX
XX WPI; 1988-265361/38.

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XX Prodn. of human manganese superoxidizedismutase peptide(s) - and DNA coding
PT sequences, for control and diagnosis of e.g. inflammatory diseases.
XX
XX Disclosure; Page ?; 57pp; German.
XX
CC The patent is for polypeptides, esp. non-glycosylated, having the
CC enzymatic, biological and immunological properties of hMnSOD that are
CC prep'd. by genetic engineering methods. Also new are DNA sequences
CC encoding all or part of the polypeptides and replicating vectors,
CC expression plasmids and transformed host cells contg. these sequences.
CC hMnSOD catalyses disproportionation of the superoxide radical and can be
CC used in the prevention, diagnosis and treatment of inflammatory,
CC degenerative, neoplastic and rheumatoid disorders; for wound healing; in
CC autoimmune disease and in organ transplantation. It can also be used to
CC improve the storage stability of liq. and solid foods. Oligo VIIa
CC (XhoI/XbaI) (AAN81222) was ligated to oligo VIb (XbaI/NotI) (AAN81223)
CC and then used to produce cDNA encoding the entire hMnSOD of formula VIIa
CC and formula VIIb (AAN81225). (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 600 BP; 173 A; 133 C; 150 G; 144 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AAN81224 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
Db 4 AAGGACCTCTTGGCCAGACTTGCATACGACTGCGTGTCTAGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAATTCATGCATTCGACCACTCT 87
RESULT 26
AAN81219
ID AAN81219 standard; cDNA; 600 BP.
XX
XX AAN81219;
XX
XX 25-MAR-2003 (revised)
DT 03-OCT-1990 (first entry)
XX
DE Sequence of Formula IIb encoding modified portion of human manganese
DE superoxide dismutase (hMnSOD).
XX
XX Human manganese superoxide dismutase derivative; clone BS8; formula IIb;
KW enzyme; EC-1.15.1.1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 4..600
FT /*tag= a
XX
XX EP282899-A.
XX
XX 21-SEP-1988.
XX
XX 10-MAR-1988; 88EP-00103754.
XX
XX 14-MAR-1987; 87DE-03708306.
PR 26-MAY-1987; 87DE-03717695.
PR 10-JUL-1987; 87DE-03722884.
PR 24-DEC-1987; 87DE-03744038.
XX

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PA (BOEH ) BOEHRINGER INGELHEIM.
XX
XX Heckl K, Spevak W, Ostermann E, Zophel A, Krystek E;
PI Maurerfogy I, Michcascata Wu, Stralow C;
XX
XX WPI; 1988-265361/38.
DR P-PSDB; AAP80603.
XX
PT Prodn. of human manganese superoxidizedismutase peptide(s) - and DNA coding
PT sequences, for control and diagnosis of e.g. inflammatory diseases.
XX
XX Disclosure; Page ?; 57pp; German.
XX
XX The patent is for polypeptides, esp. non-glycosylated, having the
XX enzymatic, biological and immunological properties of hMnSOD that are
XX prep'd. by genetic engineering methods. Also new are DNA sequences
XX encoding all or part of the polypeptides and replicating vectors,
XX expression plasmids and transformed host cells contg. these sequences.
XX hMnSOD catalyses disproportionation of the superoxide radical and can be
XX used in the prevention, diagnosis and treatment of inflammatory,
XX degenerative, neoplastic and rheumatoid disorders; for wound healing; in
XX autoimmune disease and in organ transplantation. It can also be used to
XX improve the storage stability of liq. and solid foods. AAN81219 is
XX derived from Formula I (AAN81826). (Updated on 25-MAR-2003 to correct PR
XX field.)
SQ Sequence 600 BP; 172 A; 135 C; 150 G; 143 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.000917 Length: 600
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
Gaps: 0
US-09-987-190-2 (1-30) x AAN81219 (1-600)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSergly 20
Db 4 AAGGACCTCTTGGCCAGACTTGCATACGACTGCGTGTCTAGAACACACATCAATGCT 63
QY 21 GlnIleAsnGluIle***TyrThr 28
Db 64 CAATTCATGCATTCGACCACTCT 87
RESULT 27
AAQ94278
ID AAQ94278 standard; cDNA; 600 BP.
XX
XX AAQ94278;
XX
XX 25-MAR-2003 (revised)
DT 23-MAY-1996 (first entry)
XX
DE Human manganese superoxide dismutase (Gln29) coding sequence.
XX
XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
KW autoimmune disease; rheumatoid arthritis; neoplasia; emphysema;
KW osteoarthritis; wound healing; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT CDS 1..600
FT /*tag= a
FT /product= "Met hMn-SOD(Gln29)"
FT /note= "the first 31 codons are provided by a synthetic
FT linker sequence"
XX
XX EP676472-A1.
XX

```


PD 11-OCT-1995.
 XX PF 10-MAR-1988; 95EP-00107460.
 XX PR 14-MAR-1987; 87DE-03708306.
 PR 26-MAY-1987; 87DE-03717695.
 PR 10-JUL-1987; 87DE-03722884.
 PR 24-DEC-1987; 87DE-03744038.
 XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX PI Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E,
 PI Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;
 XX WPI; 1995-346092/45.
 DR WPI; 1995-346092/45.
 XX PT Genes encoding recombinant human manganese superoxide dismutase - for
 PT treatment, prevention and diagnosis of inflammatory diseases.
 XX PS Claim 8; Page 17-18; 54pp; German.
 CC The present sequence codes for a Met residue followed by the 198 amino
 CC acid long hMn-SOD mature polypeptide having a Gln residue at position 29.
 CC The cDNA can be inserted into expression vectors containing appropriate
 CC signal sequences, etc. for expression of recombinant hMn-SOD. The N-
 CC terminal Met residue can be removed, e.g. by treatment with CNBr or CNCl.
 CC Mature hMn-SOD is useful for treating, preventing or diagnosing
 CC inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
 CC healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX SQ Sequence 600 BP; 172 A; 134 C; 150 G; 144 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.000917 Length: 600
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 0
 US-09-987-190-2 (1-30) x AAQ94278 (1-600)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 4 AAGCAGCTCTTGGCCAGACTGCGCATACGACTACGCTGCTAGAACACACATCATGCT 63
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 64 CAAATCATGCATATGCACCACTCT 87
 RESULT 28
 AAQ94271
 ID AAQ94271 standard; cDNA; 600 BP.
 XX AC AAQ94271;
 XX DT 25-MAR-2003 (revised)
 DT 17-MAY-1996 (first entry)
 XX DE Human manganese superoxide dismutase (lys29) coding sequence.
 XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KM osteoarthritis; wound healing; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..600
 FT /**tag= a
 FT /product= "Met_hMn-SOD (lys29)"
 XX CDS

EN E676472-A1.
 XX PD 11-OCT-1995.
 XX PF 10-MAR-1988; 95EP-00107460.
 XX PR 14-MAR-1987; 87DE-03708306.
 PR 26-MAY-1987; 87DE-03717695.
 PR 10-JUL-1987; 87DE-03722884.
 PR 24-DEC-1987; 87DE-03744038.
 XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX PI Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E,
 PI Maurer-Fogy I, Wiche-Castanon M, Stratowa C, Hauptmann R;
 XX WPI; 1995-346092/45.
 DR WPI; 1995-346092/45.
 DR P-PSDB; AAR75191.
 XX PT Genes encoding recombinant human manganese superoxide dismutase - for
 PT treatment, prevention and diagnosis of inflammatory diseases.
 XX PS Claim 8; Page 6; 54pp; German.
 CC The present sequence codes for a Met residue followed by the 198 amino
 CC acid long hMn-SOD mature polypeptide having a Lys residue at position 29.
 CC The cDNA can be inserted into expression vectors containing appropriate
 CC signal sequences, etc. for expression of recombinant hMn-SOD. The N-
 CC terminal Met residue can be removed, e.g. by treatment with CNBr or CNCl.
 CC Mature hMn-SOD is useful for treating, preventing or diagnosing
 CC inflammatory, degenerative, neoplastic and rheumatic disorders; in wound
 CC healing and in autoimmune diseases. (Updated on 25-MAR-2003 to correct PF
 CC field.)
 XX SQ Sequence 600 BP; 173 A; 134 C; 150 G; 143 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.000917 Length: 600
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 0
 US-09-987-190-2 (1-30) x AAQ94271 (1-600)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 4 AAGCAGCTCTTGGCCAGACTGCGCATACGACTACGCTGCTAGAACACACATCATGCT 63
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 64 CAAATCATGCATATGCACCACTCT 87
 RESULT 29
 AAQ94272
 ID AAQ94272 standard; cDNA; 600 BP.
 XX AC AAQ94272;
 XX DT 25-MAR-2003 (revised)
 DT 17-MAY-1996 (first entry)
 XX DE Human manganese superoxide dismutase (Gln29) coding sequence.
 XX hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KM autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KM osteoarthritis; wound healing; ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..600
 FT /**tag= a
 FT /product= "Met_hMn-SOD (lys29)"
 XX CDS

XX Homo sapiens.
OS
XX
XX EP462836-A.
XX
XX PD 27-DEC-1991.
XX
XX PF 20-JUN-1991; 91EP-00305596.
XX
XX PR 20-JUN-1990; 90JP-00159925.
XX PR 19-OCT-1990; 90JP-00279286.
XX
XX PA (MITK) MITSUI TOATSU CHEM INC.
XX
XX PI Takahashi S, Makino T, Asanagi M, Yoshino C;
XX
XX DR WPI; 1992-001187/01.
XX DR P-PSDB; MAR20015.
XX
XX PT New recombinant vector plasmid - expresses human manganese, superoxide
XX PT dismutase, used as antiinflammatory agent.
XX
XX PS Disclosure; Fig 8; 22pp; English.
XX
XX CC A vector was constructed contg. tac/P1 ligated promoter which has this
XX CC human Mn-SOD structural gene. The gene encodes modified human Mn-SOD in
XX CC which the 59th isoleucine is converted to threonine
XX
SQ Sequence 609 BP; 171 A; 148 C; 157 G; 133 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000935 Length: 609
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x AAQ20194 (1-609)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 6 AAGGACAGCCTCCCTGACCTGCTACGACTAGCGGCCCTGGAACCTCAATCAACGCG 65
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 66 CAGATCATGCAGCTGCACACACG 89

RESULT 32
ABT09580
ID ABR09580 standard; DNA; 666 BP.
XX
XX AC ABR09580;
XX
XX DT 05-DEC-2002 (first entry)
XX
XX DE Phase-1 Rat CT gene SEQ ID No 668.
XX
XX KM Rat; toxicity study; rat toxic response gene; toxicological response;
XX KM drug development; phase-1 rat CT gene; ds.
XX
XX OS Rattus sp.
XX OS
XX PN WO200266682-A2.
XX PD 29-AUG-2002.
XX
XX PF 29-JAN-2002; 2002WO-US002935.
XX
XX PR 29-JAN-2001; 2001US-0264933P.
XX PR 26-JUL-2001; 2001US-0308151P.
XX
XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX
XX PI Farris G, Hicken SH, Farr SB;
XX
XX DR WPI; 2002-674961/72.
XX
XX PT Evaluating the toxicity of an agent, useful in drug development or in
XX PT determining toxicological responses to a new drug, by determining the
XX PT expression of rat toxicologically relevant genes in the test animal in
XX PT response to the test agent.
XX
XX PS Disclosure; Page 270; 388pp; English.
XX
XX CC The invention relates to a method used for evaluating the toxicity of an
XX CC agent comprising determining the expression of a rat toxic response
XX CC gene(s) in the test animal in response to the agent. The method is useful
XX CC in drug development, particularly for conducting toxicity studies and
XX CC analysis before a new drug or compound is approved for human consumption
XX CC or use. The method is also useful in determining toxicological responses
XX CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT
XX CC gene of the invention
XX
SQ Sequence 666 BP; 172 A; 164 C; 182 G; 146 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 0.00105 Length: 666
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x ABR09580 (1-666)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 88 AAGGACAGCCTCCCTGACCTGCTACGACTAGCGGCCCTGGAACCTCAATCAACGCG 147
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 148 CAGATCATGCAGCTGCACACACG 171

RESULT 33
AAZ39781
ID AAZ39781 standard; DNA; 681 BP.
XX
XX AC AAZ39781;
XX
XX DT 06-MAR-2000 (first entry)
XX
XX DE Human manganese superoxide dismutase (MnSOD) mutant protein DNA.
XX
XX KM Manganese superoxide dismutase; MnSOD; ECsOD; proteoglycan; human;
XX KM endothelial; oxidative damage; pulmonary inflammatory injury; cancer;
XX KM lung disease; hypoxia; ischemia; reperfusion injury; arthritis;
XX KM hyperoxia; atherosclerosis; lupus erythematosus; hypertension;
XX KM neutrophil-mediated inflammation; mutant; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9958547-A1.
XX PD 18-NOV-1999.
XX
XX PF 06-MAY-1999; 99WO-US009921.
XX
XX PR 08-MAY-1998; 98US-00075019.
XX
XX PA (WEBB-) WEBB-MARING INST BIOMEDICAL RES.
XX
XX PI Mccord JM, Gao B, Flores SC;
XX
XX DR WPI; 2000-062283/05.

XX	PN	BB305796-A.	
XX	PD	16-MAR-1987.	
XX	PF	20-NOV-1986;	86BE-00905796.
XX	PR	22-NOV-1985;	85US-00801051.
XX	PR	22-NOV-1985;	85US-00801090.
XX	PR	12-SEP-1986;	86US-00907051.
XX	PA	(BIOT-) BIO-TECHNOL GEN.	
XX	DR	WPI; 1987-101441/15.	
XX	DR	P-PsDB; AAN71370.	
XX	PT	New DNA coding for polypeptide of human manganese superoxidisedismutase -	
XX	PT	useful e.g. for treating inflammation, and new expression vectors and	
XX	PS	transformed cells.	
XX	PS	Disclosure; Fig 1; 46pp; French.	
XX	CC	This purified cDNA encodes both prepro- and mature-manganese superoxide	
XX	CC	dismutase (MSOD). It is one strand of a double stranded molecule	
XX	CC	contained in a recombinant vehicle. The MSOD produced catalyses the	
XX	CC	reaction of hydrogen ions and the SOD radical anion to form hydrogen	
XX	CC	peroxide and water. It is useful in veterinary and pharmaceutical	
XX	CC	compounds. for e.g. reducing lesions of reperfusion following ischaemia, to	
XX	CC	prolong survival time isolated organs and for treating inflammation. See	
XX	CC	also AAN71371-72. (Updated on 10-MAR-2003 to add missing OS field.)	
XX	CC	(Updated on 25-MAR-2003 to correct PR field.)	
XX	XX	Sequence 813 BP; 218 A; 204 C; 213 G; 178 T; 0 U; 0 Other;	
XX	XX	Alignment Scores:	
XX	XX	Pred. No.:	0.00136
XX	XX	Score:	74.00
XX	XX	Percent Similarity:	78.57%
XX	XX	Best Local Similarity:	42.86%
XX	XX	Query Match:	51.03%
XX	XX	DB:	1
XX	XX	Gaps:	0
XX	XX	US-09-987-190-2 (1-30) x AAN71370 (1-813)	
XX	QY	1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaIrrhGluProTyrIleSerGly 20	
XX	Db	115 AAGCAAGAGCCTCCCGACCTGCGCTACGACTACGGCGCCTCGAAGCCTCAGATCAAGCG 174	
XX	QY	21 GlnIleAsnGlnIle**TyrThr 28	
XX	Db	175 CAGATCATGCAAGCTGCACCAAGC 198	
XX	XX	RESULT 35	
XX	ID	AAN81158	
XX	XX	AAN81158 standard; cDNA; 813 BP.	
XX	AC	AAN81158;	
XX	XX	22-OCT-1990 (first entry)	
XX	DE	cDNA encoding human manganese superoxide dismutase.	
XX	XX	Human manganese superoxide dismutase; ds cDNA; oxygen free radicals.	
XX	OS	Homo sapiens.	
XX	XX	Key	Location/Qualifiers
XX	FT	CDS	43..711
XX	FT	FT	/*tag= a
XX	XX	EP284105-A.	
XX	XX	28-SEP-1988.	

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XX 25-MAR-1988; 88EP-00104860.
PF 27-MAR-1987; 87US-00032734.
XX 26-FEB-1988; 88US-00161117.
PR 26-FEB-1988; 88US-00161117.
XX (BIOT-) BIO-TECHNOLOGY GEN.
PA
XX Hartman JR, Beck Y, Nimrod A;
XX WPI: 1988-272584/39.
DR P-PSDB; AAP80551.
XX
XX Recombinant human manganese superoxidisedismutase - used for treating e.g.
PT reperfusion injury, inflammation, arthritis, bronchial pulmonary
PT dysplasia or lung fibrosis.
XX
PS Disclosure; Page 7; 46pp; English.
XX The cDNA encodes human manganese superoxide dismutase, and is inserted
CC into a plasmid, eg pMSB-4 (ATCC 53250)
CC
XX
SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00136 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 1 Gaps: 0

US-09-987-190-2 (1-30) x AAN81158 (1-813)

QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 115 AAGCAGACGCTCCCGACTGCGCTACGACTACGCGCGCCCTGGAACCTCACATCAACGCG 174
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 175 CAGATCATGCACTGCAACACACAGC 198

RESULT 36
AAQ53193
ID AAQ53193 standard; cDNA; 813 BP.
XX
AC AAQ53193;
XX
DT 25-MAR-2003 (revised)
DT 21-JUN-1994 (first entry)
XX
DE MSOD cDNA.
XX
KW MSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion;
KW injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
KW ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 43..711
XX FT /*tag= a
XX FT /product= "MSOD"
XX
XX US5270195-A.
XX
XX 14-DEC-1993.
XX
XX 10-JUL-1992; 92US-00912213.
XX
XX 22-NOV-1986; 85US-00801090.
XX 12-SEP-1986; 86US-00907051.
XX 29-OCT-1986; 86IE-00002851.
```

```
ER 27-MAR-1987; 87US-00032734.
PR 13-DEC-1989; 89US-00453057.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
PA
XX Beck Y, Hartman JR;
XX WPI: 1993-404931/50.
DR P-PSDB; AAR44801.
XX
XX Expression plasmid in Escherichia coli host system - encodes human
PT manganese superoxidisedismutase analogue, useful for e.g. treating
PT inflammation.
XX
PS Claim 1; Fig 1a-1c; 27pp; English.
XX
XX The sequence encodes a maganese superoxide dismutase which can be used to
CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide
CC and molecular oxygen. It can be used to reduce reperfusion injury
CC following ischaemia and prolong the survival of excised organs. It can
CC also me used as a long acting anti-inflammatory drug. (Updated on 25-MAR-
CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
XX
SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.00136 Length: 813
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 2 Gaps: 0

US-09-987-190-2 (1-30) x AAQ53193 (1-813)

QY 1 LysTyrSerLeuPProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 115 AAGCAGACGCTCCCGACTGCGCTACGACTACGCGCGCCCTGGAACCTCACATCAACGCG 174
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 175 CAGATCATGCACTGCAACACACAGC 198

RESULT 37
AAT15589
ID AAT15589 standard; cDNA; 813 BP.
XX
AC AAT15589;
XX
DT 25-MAR-2003 (revised)
DT 06-APR-1996 (first entry)
XX
DE Human manganese superoxide-dismutase cDNA.
XX
XX Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
KW Escherichia coli; plasmid pMSB-4; N-terminal truncation; cloning;
KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;
KW synovial inflammation; arthritis; lung fibrosis; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 43..711
XX FT /*tag= a
XX FT /product= "Manganese superoxide-dismutase"
XX FT /note= "Ec-1.15.1.1"
XX FT sig_peptide 43..114
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XX EP691401-A1.
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KM Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 XX inflammation; reperfusion injury; therapy; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..711
 FT sig_peptide /*tag= a
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 FT /*tag= b
 FT mat_peptide 115..708
 FT /*tag= c
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 XX WO911088-A1.
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 XX 18-MAR-1999.
 XX
 XX 10-SEP-1998; 98WO-US018842.
 XX
 XX 10-SEP-1997; 97US-00927230.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 XX Nick HS, Silverman DN;
 XX
 XX WPI: 1999-229242/19.
 XX P-PSDB; AAW98169.
 XX
 XX New recombinant human manganese superoxide dismutase proteins.
 XX
 XX Disclosure: Page 52-53; 61pp; English.
 XX
 CC This cDNA sequence codes for human manganese superoxide dismutase
 CC (MnSOD; see AAW98169). Novel MnSOD proteins having catalytic activity
 CC which differs from this natural hMnSOD are claimed. The modified proteins
 CC exhibit reduced or no product inhibition, or have greater activity, or
 CC both, compared to natural hMnSOD. The modifications involve one or amino
 CC acid substitutions within the active site of the enzyme, especially at
 CC residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
 CC His-163 (see also AAW98171-77). Nucleic acids encoding the modified
 CC hMnSOD proteins are also claimed. The modified hMnSOD proteins, or
 CC expression vectors in which modified hMnSOD nucleic acid is linked to a
 CC promoter (preferably mammalian), can be used to protect a cell line from
 CC damage caused by superoxide radicals (claimed). They can also be used to
 CC treat subjects suffering from, or at risk of, cytotoxicity caused by
 CC superoxide radicals (claimed). As such, they can be used as antioxidants
 CC in the treatment of a variety of disorders, including inflammation
 CC (claimed), reperfusion injury following ischemia (claimed), and cellular
 CC damage caused by chemotherapeutic agents
 XX
 SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 0.00136 Length: 813
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 0
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 DB 115 AAGGACAGCCTCCCGACCTGCGCTACGAGCGCCCTGGAACCTCAGCTCAACGCG 174
 QY 21 GlnIleAsnGluIle**TyrThr 28
 DB 175 CAGATCATGCACTGACACACAGC 198
 RESULT 40
 AAA63891

ID AAA63891 standard; cDNA; 813 BP.
 XX
 AC AAA63891;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cDNA encoding a human manganese superoxide dismutase.
 XX
 KW Human; manganese superoxide dismutase; hMn SOD; superoxide radical;
 KW superoxide radical damage; cytotoxicity; inflammation; ischemia;
 KW reperfusion injury; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 43..711
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 FT /product= "manganese superoxide dismutase"
 FT /note= "Xaa is Gln or Glu"
 FT sig_peptide 43..114
 FT /*tag= b
 FT mat_peptide 115..708
 FT /*tag= c
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 XX US6107070-A.
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 XX 22-AUG-2000.
 XX
 XX 10-SEP-1998; 98US-00151052.
 XX
 XX 10-SEP-1997; 97US-00927230.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 XX Silverman DN, Nick HS;
 XX
 XX WPI: 2000-578537/54.
 XX P-PSDB; AAB08204.
 XX
 XX Novel human manganese superoxide dismutase protein useful as antioxidant
 XX for treating cytotoxicity caused by superoxide radicals, inflammation and
 XX reperfusion injury following ischemia.
 XX
 XX Disclosure: Col 25-26; 27pp; English.
 XX
 CC The present sequence encodes a human manganese superoxide dismutase
 CC protein (hMn SOD). The specification describes a modified hMn SOD which
 CC has a catalytic activity which differs from natural hMn SOD in that it
 CC exhibits reduced or no product inhibition compared to natural hMn SOD.
 CC The natural hMn SOD is especially modified with one or more substitutions
 CC in amino acids 26, 30, 34, 74, 143, 159, 161 and 163. The modified hMn
 CC SOD is useful for protecting a cell from damage caused by superoxide
 CC radicals and for treating a subject suffering from cytotoxicity caused by
 CC superoxide radicals. The protein is useful for treating inflammation and
 CC reperfusion injury following ischemia
 XX
 SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 0.00136 Length: 813
 Score: 74.00 Matches: 12
 Percent Similarity: 78.57% Conservative: 10
 Best Local Similarity: 42.86% Mismatches: 6
 Query Match: 51.03% Indels: 0
 DB: Gaps: 0
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 DB 115 AAGGACAGCCTCCCGACCTGCGCTACGAGCGCCCTGGAACCTCAGCTCAACGCG 174

Qy 21 Glnleanglule**TyrThr 28
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Db 175 CAGATCATGCACTGACACACAC 198

Search completed: August 31, 2004, 18:17:57
Job time : 440 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 20:09:53 ; Search time 408 Seconds

(without alignments)
361.870 Million cell updates/sec

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Perfect score: 145
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Ygapop 10.0 , Ygapext 0.5
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Searched: 3237270 seqs, 2460713050 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	79	54.5	812	15	US-10-109-670-4	Sequence 4, Appl
2	79	54.5	2217	13	US-10-424-599-90403	Sequence 90403, A
3	77	53.1	600	9	US-09-738-626-3227	Sequence 3227, Ap
4	77	53.1	987	13	US-10-424-599-90405	Sequence 90405, A
5	77	53.1	1143	9	US-09-818-564-1	Sequence 1, Appl
6	77	53.1	3309400	9	US-09-738-626-1	Sequence 1, Appl
7	74	51.0	224	9	US-09-960-352-5895	Sequence 5895, Ap
8	74	51.0	325	9	US-09-960-352-5895	Sequence 3021, Ap
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10	74	51.0	424	9	US-09-960-352-5895	Sequence 14744, A
11	74	51.0	552	17	US-10-752-791-1	Sequence 1, Appl
12	74	51.0	666	17	US-10-404-460-256	Sequence 256, Ap
13	74	51.0	829	17	US-10-641-643-1348	Sequence 1348, Ap
14	74	51.0	972	14	US-10-044-090-835	Sequence 836, Ap
15	74	51.0	996	15	US-10-198-846-13503	Sequence 13503, A
16	74	51.0	1026	9	US-09-954-456-1822	Sequence 1822, Ap
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22	74	51.0	1067	10	US-09-971-4298-22	Sequence 22, Appl
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30	71	49.0	721	9	US-09-987-190-8	Sequence 8, Appl
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32	70	48.3	1230025	16	US-10-289-762-1	Sequence 1, Appl
33	68	46.9	6329	15	US-10-156-761-5397	Sequence 5397, Ap
34	68	46.9	2731748	17	US-10-297-465A-1	Sequence 1, Appl
35	68	46.9	9025608	15	US-10-156-761-1	Sequence 1, Appl
36	67	46.2	597	9	US-09-727-8558-6	Sequence 6, Appl
37	67	46.2	1295	16	US-10-310-154-294	Sequence 294, Ap
38	67	46.2	1830121	15	US-10-329-960-1	Sequence 1, Appl
39	67	46.2	1830121	16	US-10-329-960-1	Sequence 1, Appl
40	66	45.5	669	9	US-09-727-8558-4	Sequence 4, Appl
41	66	45.5	838	9	US-09-974-300-2052	Sequence 2052, Ap
42	62	42.8	728	15	US-10-109-670-3	Sequence 3, Appl
43	62	42.8	767	9	US-09-070-927A-425	Sequence 425, Ap
44	61	42.1	894	15	US-10-247-671-122	Sequence 122, Ap
45	61	42.1	1235	16	US-10-398-221-1367	Sequence 1367, Ap

ALIGNMENTS

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US-10-109-670-4
; Sequence 4, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUO et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 4
; LENGTH: 812
; TYPE: DNA
; ORGANISM: Malassezia furfur
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(812)
; OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
US-10-109-670-4

Alignment Scores: 9.82e-05 Length: 812
Pred. No.: 45

Score: 79.00 Matches: 15
Percent Similarity: 70.37% Conservative: 4
Best Local Similarity: 55.56% Mismatches: 8
Query Match: 54.48% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-109-670-4 (1-812)

QY 1 TySerLeuProGluLeuAspTYRGIuPheserAlaThrGIuProTYRileserGIyGln 20
DB 74 AGGTACGCGTGGCGCGCGCTGACTACGAGCGCGCTCGAGCGCGGCGATCTCGGCG 133

QY 21 IleAsnGluIle**TYR 27
DB 134 GAGATCATGGAGACGACACTAC 154

RESULT 2

US-10-424-599-90403
; Sequence 90403, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 90403
; LENGTH: 2217
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52646C.1
US-10-424-599-90403

Alignment Scores:
Pred. No.: 0.000362 Length: 2217
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-424-599-90403 (1-2217)

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DB 1142 TACGCGCTCCCGATCTGGATTACGACTATGGCGCTCGAGCCAGCACAAGCGCGGAA 1201

QY 22 IleAsnGluIle**TYR 27
DB 1202 ATCATGAGCTGCACAC 1219

RESULT 3

US-09-738-626-3227
; Sequence 3227, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3227
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3227

Alignment Scores:
Pred. No.: 0.000156 Length: 600
Score: 77.00 Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-738-626-3227 (1-600)

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QY 22 IleAsnGluIle**TYRThr 28
DB 70 ATCATGAGCTTACCACTCC 90

RESULT 4
US-10-424-599-90405/c
; Sequence 90405, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 90405
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52648C.1
US-10-424-599-90405

Alignment Scores:
Pred. No.: 0.000298 Length: 987
Score: 77.00 Matches: 13
Percent Similarity: 76.92% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 6
Query Match: 53.10% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-424-599-90405 (1-987)

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DB 805 TACGCGCTCCCGATCTGGATTACGACTATGGCGCACTCGAGCCAGCACAAGCGCGGAGAC 746

QY 22 IleAsnGluIle**TYR 27

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Db          745 ATCATGAGCTTCACCACTCC 728
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RESULT 5
US-09-818-564-1
; Sequence 1, Application US/09818564
; Patent No. US20020137151A1
; GENERAL INFORMATION:
; APPLICANT: MERKAM, MURIEL
; APPLICANT: GUYONVARCH, ARNEL
; APPLICANT: MAREX, ACHIM
; TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
; TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
; FILE REFERENCE: 21123/27841/MAS
; CURRENT APPLICATION NUMBER: US/09/818,564
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 09/373,731
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Corynebacterium melassecola
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (338)..(937)
; OTHER INFORMATION: ATCC 17965
US-09-818-564-1

Alignment Scores:
Pred. No.: 0.000361      Length: 1143
Score: 77.00             Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10%      Indels: 0
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DB: 9

US-09-987-190-2 (1-30) x US-09-818-564-1 (1-1143)

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QY      22 IleAsnGluIle***TyrThr 28
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RESULT 6
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: IATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/37484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
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; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Alignment Scores:
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Score: 77.00             Matches: 13
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 48.15% Mismatches: 7
Query Match: 53.10%      Indels: 0
                        Gaps: 0
DB: 9

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          |||          :||
QY      22 IleAsnGluIle***TyrThr 28
          |||          :||
Db      3126461 ATCATGAGCTTCACCACTCC 3126481
          |||          :||

RESULT 7
US-09-960-352-5895
; Sequence 5895, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengping
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5895
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 25-LIB34-057-Q1-E1-G1
US-09-960-352-5895

Alignment Scores:
Pred. No.: 0.000157      Length: 224
Score: 74.00             Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03%      Indels: 0
                        Gaps: 0
DB: 9

US-09-987-190-2 (1-30) x US-09-960-352-5895 (1-224)

QY      1  LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
          |||          :||
Db      140 AAGCAGAGCCTCCCGGACCTGCGTACGACTACGCGCGCTTCGAGCGGACATCAACGCG 199
          |||          :||
QY      21 GluIleAsnGluIle***TyrThr 28
          |||          :||
Db      200 CAGATCATGAGCTTCACCACTCC 223
          |||          :||

RESULT 8
US-09-960-352-3021
; Sequence 3021, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
```

```

; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3021
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 13-LIB34-076-Q1-E1-D1
US-09-960-352-3021

Alignment Scores:
Pred. No.: 0.00019 Length: 259
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-960-352-3021 (1-259)

CY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 142 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCTGGACCGCACATCAACCG 201
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CY 21 GlnIleAsnGluIle**TyrThr 28
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 CAGATCATGCACTGCACACACAGC 225
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-09-993-333-11
; Sequence 11, Application US/09993333
; Patent No. US20020156040A1
; GENERAL INFORMATION:
; APPLICANT: Oberley, Larry Wayne
; APPLICANT: Weydert, Christine J.
; APPLICANT: Smith, Benjamin Barnes
; TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using antis
; FILE REFERENCE: 875.042US1
; CURRENT APPLICATION NUMBER: US/09/993,333
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,328
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-993-333-11

Alignment Scores:
Pred. No.: 0.000255 Length: 325
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-993-333-11 (1-325)

CY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCTGGACCGCACATCAACCG 172
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CY 21 GlnIleAsnGluIle**TyrThr 28
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB: 9 Gaps: 0
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Db 173 CAGATCATGCACTGCACACAGC 196

RESULT 10
US-09-960-352-14744
; Sequence 14744, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14744
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 63-LIB3057-022-Q1-K1-H4
US-09-960-352-14744

Alignment Scores:
Pred. No.: 0.00036 Length: 424
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-960-352-14744 (1-424)

CY 1 LysTySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 AAGCAGACGCTCCCGACCTGCGCTACGACTACGCGCCCTGGACCGCACATCAACCG 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CY 21 GlnIleAsnGluIle**TyrThr 28
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 CAGATCATGCACTGCACACAGC 204
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-10-752-791-1
; Sequence 1, Application US/10752791
; Publication No. US20040152115A1
; GENERAL INFORMATION:
; APPLICANT: Anziano, Paul Q.
; TITLE OF INVENTION: Manganese Superoxide Dismutase Exon 3-Deleted Isoforms
; FILE REFERENCE: 53073-0001-US
; CURRENT APPLICATION NUMBER: US/10/752,791
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/623,025C
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/075,948
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: PCT/US99/04129
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(552)
; OTHER INFORMATION: Isoform of MnSOD E3(-)
US-10-752-791-1

Alignment Scores:
Pred. No.: 0.000508 Length: 552
```

Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 17 Gaps: 0
US-09-987-190-2 (1-30) x US-10-752-791-1 (1-552)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 73 AAGCAGACGCTCCCGACCTGACACTAGCGCCCTGAACTCATCATCAACGG 132
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 133 CAGATCATGACGCTGCACCAACG 156
RESULT 12
US-10-404-460-256
; Sequence 256, Application US/10404460
; Publication No. US20040076974A1
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Klier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Usha
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Liver Necrosis Predictive Genes
; FILE REFERENCE: 2874-022
; CURRENT APPLICATION NUMBER: US/10/404,460
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/369,287
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: predictive genes for liver necrosis
; NAME/KEY: misc feature
; LOCATION: 4, 666
; OTHER INFORMATION: n = A,T,C or G
US-10-404-460-256
Alignment Scores:
Pred. No.: 0.000648 Length: 666
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 17 Gaps: 0
US-09-987-190-2 (1-30) x US-10-404-460-256 (1-666)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 88 AAGCAGACGCTCCCGACCTGACACTAGCGCCCTGAACTCATCATCAACGG 147
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 148 CAGATCATGACGCTGCACCAACG 171
RESULT 13
US-10-641-643-1348
; Sequence 1348, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 934710
SEQUENCE DESCRIPTION: SEQ ID NO: 1348 :
US-10-641-643-1348
Alignment Scores:
Pred. No.: 0.000861 Length: 829
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 17 Gaps: 0
US-09-987-190-2 (1-30) x US-10-641-643-1348 (1-829)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 139 AAGCAGACGCTCCCGACCTGACACTAGCGCCCTGAACTCATCATCAACGG 198
QY 21 GlnIleAsnGluIle***TyrThr 28
DB 199 CAGATCATGACGCTGCACCAACG 222
RESULT 14
US-10-044-090-836
; Sequence 836, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 836
; LENGTH: 972
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 010001CB1
US-10-044-090-836

Alignment Scores:
Pred. No.: 0.00106 Length: 972
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x US-10-044-090-836 (1-972)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 166 AAGCAGACGCTCCCGACCTGCGCTGAGCTAGCAGCGCGCCCTGGAACCTCACATCAAGCG 225
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 226 CAGATCATGCGCTGCACCAAGC 249

RESULT 15
US-10-198-846-13503
; Sequence 13503, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinhmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13503
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13503

Alignment Scores:
Pred. No.: 0.00109 Length: 996
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-198-846-13503 (1-996)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 163 AAGCAGACGCTCCCGACCTGCGCTGAGCTAGCAGCGCGCCCTGGAACCTCACATCAAGCG 222
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 223 CAGATCATGCGCTGCACCAAGC 246

RESULT 16
US-09-954-456-1822
; Sequence 1822, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
```

```

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1822
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1822

Alignment Scores:
Pred. No.: 0.00114 Length: 1026
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-954-456-1822 (1-1026)
QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
Db 77 AAGCAGACGCTCCCGACCTGCGCTGAGCTAGCAGCGCGCCCTGGAACCTCACATCAAGCG 136
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 137 CAGATCATGCGCTGCACCAAGC 160

RESULT 17
US-10-342-887-509
; Sequence 509, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yidong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
```



```
/ SEQ ID NO 1627
/ LENGTH: 1492
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017051
US-09-917-800A-1627

Alignment Scores:
Pred. No.: 0.00185 Length: 1492
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x US-09-917-800A-1627 (1-1492)
QY 1 LysTySerLeuProGluIleuAspTyrGluIleuSerAlaThrGluProTyrIleSerGly 20
Db 141 AAGCAGAGCTCTCCCTGACCTTACGACTATGCGCGTGGAGCGCACATTAAAGCG 200
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 201 CAGATCATGCAGCTGCACCAACAGC 224

RESULT 24
US-10-342-887-267
/ Sequence 267, Application US/10342887
/ Publication No. US20040058340A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: He, Hongyue
/ APPLICANT: Linsley, Peter S.
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Christopher J.
/ APPLICANT: Van 't Veer, Laura Johanna
/ APPLICANT: Van de Vijver, Marc J.
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-188-999
/ CURRENT APPLICATION NUMBER: US/10/342,887
/ CURRENT FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: 60/298,918
/ PRIOR FILING DATE: 2001-06-18
/ PRIOR APPLICATION NUMBER: 60/380,710
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 10/172,118
/ PRIOR FILING DATE: 2002-06-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 267
/ LENGTH: 1984
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-342-887-267

Alignment Scores:
Pred. No.: 0.00267 Length: 1984
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-342-887-267 (1-1984)
QY 1 LysTySerLeuProGluIleuAspTyrGluIleuSerAlaThrGluProTyrIleSerGly 20
Db 150 AAGCAGAGCTCTCCCTGACCTTACGACTATGCGCGTGGAGCGCACATTAAAGCG 209
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 210 CAGATCATGCAGCTGCACCAACAGC 233
```

```
RESULT 25
US-10-172-118-267
/ Sequence 267, Application US/10172118
/ Publication No. US20030224374A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: He, Hongyue
/ APPLICANT: Linsley, Peter
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Chris
/ APPLICANT: Van 't Veer, Laura
/ APPLICANT: Van de Vijver, Marc
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-175-999
/ CURRENT APPLICATION NUMBER: US/10/172,118
/ CURRENT FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 267
/ LENGTH: 1984
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: AL050388
/ DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-267

Alignment Scores:
Pred. No.: 0.00267 Length: 1984
Score: 74.00 Matches: 12
Percent Similarity: 78.57% Conservative: 10
Best Local Similarity: 42.86% Mismatches: 6
Query Match: 51.03% Indels: 0
DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x US-10-172-118-267 (1-1984)
QY 1 LysTySerLeuProGluIleuAspTyrGluIleuSerAlaThrGluProTyrIleSerGly 20
Db 150 AAGCAGAGCTCTCCCTGACCTTACGACTATGCGCGTGGAGCGCACATTAAAGCG 209
QY 21 GlnIleAsnGluIle**TyrThr 28
Db 210 CAGATCATGCAGCTGCACCAACAGC 233

RESULT 26
US-10-198-846-13787
/ Sequence 13787, Application US/10198846
/ Publication No. US2003009974A1
/ GENERAL INFORMATION:
/ APPLICANT: Lillie, James
/ APPLICANT: Xu, Yongyao
/ APPLICANT: Wang, Youzhen
/ APPLICANT: Steinmann, Kathleen
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
/ TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ FILE REFERENCE: MRI-049 THERAPY OF BREAST CANCER
/ CURRENT APPLICATION NUMBER: US/10/198,846
/ CURRENT FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/306,220
/ PRIOR FILING DATE: 2001-07-18
/ NUMBER OF SEQ ID NOS: 14084
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13787
/ LENGTH: 2825
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-198-846-13787
```



```
RESULT 30
US-09-987-190-8
; Sequence 8, Application US/09987190
; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutosh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikumoshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-987-190-8

Alignment Scores:
Pred. No.: 0.0026 Length: 721
Score: 71.00 Matches: 13
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 81.25% Mismatches: 1
Query Match: 48.97% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-987-190-8 (1-721)

QY 13 AlaThrGluProTyrIleSerGlyGlnIleAsnGluIle**TyrThr 28
Db 1 GCCACTGACCGTACATCATCAGCGACAAATGACGAATTCATCTACACT 48

RESULT 31
US-09-770-445-745
; Sequence 745, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: Ai, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moesener, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 745
; LENGTH: 817
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-745

Alignment Scores:
Pred. No.: 0.00469 Length: 817
Score: 70.00 Matches: 12
Percent Similarity: 76.92% Conservative: 8
Best Local Similarity: 46.15% Mismatches: 6
Query Match: 48.28% Indels: 0
DB: Gaps: 0

US-09-987-190-2 (1-30) x US-09-770-445-745 (1-817)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 48 TTACGCTTCCTGATCTTCCTTACGATTTATGCGCATTTGAAACGGCGCATTTATGAGAG 107

QY 22 IleAsnGluIle**Tyr 27
Db 108 ATCATGCGATTCATCTAC 125

RESULT 32
US-10-289-762-1
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (105001)..(120000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (120001)..(135000)
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NAME/KEY: misc feature
LOCATION: (135001)..(150000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (150001)..(165000)
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FEATURE:
NAME/KEY: misc feature
LOCATION: (180001)..(195000)
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FEATURE:
NAME/KEY: misc feature
LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (330001)..(345000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (360001)..(375000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (390001)..(405000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (420001)..(435000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (450001)..(465000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
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LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
FEATURE:
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LOCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (675601)..(690000)
/ OTHER INFORMATION: n=a or c or g or t
/ FEATURE:

Alignment Scores:
Pred. No.: 62.9 Length: 1230025
Score: 70.00 Matches: 13
Percent Similarity: 76.19% Conservative: 3
Best Local Similarity: 61.90% Mismatches: 5
Query Match: 48.28% Indels: 0
DB: 16 Gaps: 0

US-09-987-190-2 (1-30) x US-10-289-762-1 (1-1230025)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 83327 TATCTTTACCAAGTTACCTATGATGATACGCTTGAGCGCTGTAATTTCTTGAA 83386
QY 22 Ile 22
Db 83387 ATT 83389

RESULT 33
US-10-156-761-5397
/ Sequence 5397, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156,761
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 5397
/ LENGTH: 639
/ TYPE: DNA
/ ORGANISM: Streptomyces avermitilis
/ NAME/KEY: CDS
/ LOCATION: (1)..(639)
US-10-156-761-5397

Alignment Scores:
Pred. No.: 0.00804 Length: 639
Score: 68.00 Matches: 13
Percent Similarity: 73.08% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 7
Query Match: 46.90% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-156-761-5397 (1-639)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 10 TACACACTCCCTGCACTGCGCTACACACTCTCCGCGCTGCGCCCTGATCAAGCCCCGAG 69
QY 22 IleAsnGluIle**Tyr 27
Db 70 ATCATCGAGCTGCACACCAC 87

RESULT 34
```

```
US-10-297-465A-1/c
/ Sequence 1, Application US/10297465A
/ Publication No. US20040142413A1
/ GENERAL INFORMATION:
/ APPLICANT: Simpson, Andrew
/ APPLICANT: Reinach, Fernando
/ APPLICANT: Secubal, Joao
/ APPLICANT: Mediantis, Joao
/ APPLICANT: Arruda, Paulo
/ TITLE OF INVENTION: Isolated Genome of Xylella fastidiosa and Uses Thereof
/ FILE REFERENCE: FAPESP 202 US (10213376)
/ CURRENT APPLICATION NUMBER: US/10/297,465A
/ PRIOR FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: PCT/IB01/01618
/ PRIOR FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,906
/ PRIOR FILING DATE: 2001-06-17
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1
/ LENGTH: 2731748
/ TYPE: DNA
/ ORGANISM: Xylella fastidiosa
US-10-297-465A-1

Alignment Scores:
Pred. No.: 418 Length: 2731748
Score: 68.00 Matches: 13
Percent Similarity: 62.96% Conservative: 4
Best Local Similarity: 48.15% Mismatches: 10
Query Match: 46.90% Indels: 0
DB: 17 Gaps: 0

US-09-987-190-2 (1-30) x US-10-297-465A-1 (1-2731748)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 2495021 TACACCTTCCCACTCTGCTTACGCTTACGATGCGTTCGACCGCATTTGATGCGCAG 2494962
QY 22 IleAsnGluIle**TyrThr 28
Db 2494961 ACAATGAAATCCATTACACC 2494941

RESULT 35
US-10-156-761-1/c
/ Sequence 1, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILE REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156,761
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 1
/ LENGTH: 9025608
/ TYPE: DNA
/ ORGANISM: Streptomyces avermitilis
/ NAME/KEY: CDS
/ LOCATION: (4187715)
/ OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
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```
RESULT 38
US-10-329-960-1/C
; Sequence 1, Application US/10329960
; Publication No. US2003009277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10150)..(10150)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29298)..(29298)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36543)..(36543)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36551)..(36551)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36636)..(36636)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40808)..(40810)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44416)..(44416)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44905)..(44905)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44975)..(44975)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45593)..(45593)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (45732)..(45732)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (47036)..(47036)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51334)..(51334)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51602)..(51602)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51786)..(51786)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51805)..(51805)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55369)..(55369)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65309)..(65309)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65313)..(65313)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (80024)..(80024)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (100091)..(100091)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (102696)..(102696)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (105121)..(105121)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (107248)..(107248)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (117136)..(117136)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119750)..(119750)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119924)..(119924)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120038)..(120038)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: (121344) .. (121344)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122167) .. (122167)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122336) .. (122336)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131340) .. (131340)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131360) .. (131360)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (139910) .. (139910)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (140398) .. (140398)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (142750) .. (142750)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145058) .. (145058)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145171) .. (145171)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (145942) .. (145942)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (147197) .. (147197)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (150841) .. (150841)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (152500) .. (152500)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (152530) .. (152530)
OTHER INFORMATION: n equals a, t, g or c

Alignment Scores:
Pred. No.: 381 Length: 1830121
Score: 67.00 Matches: 12
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 44.44% Mismatches: 9
Query Match: 46.21% Indels: 0
DB: 15 Gaps: 0

US-09-987-190-2 (1-30) x US-10-329-960-1 (1-1830121)

QY 2 TyriserleupProginLeuaspTyrgluPheseralatrrGluProTyrlleserglYn 21
Db 1152886 TACACTCCCTCCGATTTAGGCTATGCTCCTACACATGGCTAGAACACACATTTGATGCGCA 1152827
QY 22 llaengluille***TyrThr 28

```

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Db      1152826  ACATGGAATCCATCATAGT  1152806

RESULT 39
US-10-329-670-1/c
; Sequence 1, Application US/10329670
; Publication No. US20040018503A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragment
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,670
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4747)..(4747)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9921)..(9921)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10150)..(10150)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (29298)..(29298)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36543)..(36543)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36551)..(36551)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36636)..(36636)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40808)..(40810)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4416)..(4416)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44905)..(44905)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (44975)..(44975)
; OTHER INFORMATION: n equals a, t, g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (45593)..(45593)

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/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (45732)..(45732)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (47036)..(47036)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (51334)..(51334)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (51602)..(51602)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (51786)..(51786)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (51805)..(51805)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (55369)..(55369)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (65309)..(65309)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (65313)..(65313)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (80024)..(80024)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: n equals a, t, g or c
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/ NAME/KEY: misc_feature
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/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (107248)..(107248)
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (117136)..(117136)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (119750)..(119750)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (119824)..(119824)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (120038)..(120038)
/ OTHER INFORMATION: n equals a, t, g or c

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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (121344)..(121344)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (122167)..(122167)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
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/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: n equals a, t, g or c
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/ NAME/KEY: misc_feature
/ LOCATION: (131360)..(131360)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (139910)..(139910)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (140398)..(140398)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (142750)..(142750)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
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/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: n equals a, t, g or c
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/ NAME/KEY: misc_feature
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (147197)..(147197)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (150841)..(150841)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (152500)..(152500)
/ OTHER INFORMATION: n equals a, t, g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (152530)..(152530)

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Alignment Scores:

Pred. No.:	381	Length:	1830121
Score:	67.00	Matches:	12
Percent Similarity:	66.67%	Conservative:	6
Best Local Similarity:	44.44%	Mismatches:	9
Query Match:	46.21%	Indels:	0
DB:	16	Gaps:	0

US-09-987-190-2 (1-30) x US-10-329-670-1 (1-1830121)

```

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaTrnGluProTyrIleSerGlyGln 21
DB 1152886 TACACTCTCCCTGATTAATGAGCTATGCTCAACATGCGTTAGAACACCAATTGATGCGCA 1152827

```

QY 22 lIeasngluile**TyThr 28

Db 1152826 ACAATGAAATCATCATAGT 1152806

RESULT 40

US-09-727-855B-4

; Sequence 4, Application US/09727855B

; Patent No. US20020168703A1

; GENERAL INFORMATION:

; APPLICANT: HOSHINO, Tatsuo

; APPLICANT: OTIMA, Kazuyuki

; APPLICANT: SETOGUCHI, Yutaka

; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL

; TITLE OF INVENTION: MATERIALS THEREOF

; FILE REFERENCE: C38435/111694

; CURRENT APPLICATION NUMBER: US/09/727,855B

; CURRENT FILING DATE: 2000-12-01

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 669

; TYPE: DNA

; ORGANISM: Rhodospirillum rubrum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(666)

; OTHER INFORMATION: n or X = A, C, G or T

US-09-727-855B-4

Alignment Scores:

Pred. No.: 0.0201

Score: 66.00

Percent Similarity: 67.86%

Best Local Similarity: 46.43%

Query Match: 45.52%

DB: 9

Length: 669

Matches: 13

Conservative: 6

Mismatches: 9

Indels: 0

Gaps: 0

US-09-987-190-2 (1-30) x US-09-727-855B-4 (1-669)

QY 1 lYsTySeSerleupProGluLeuAspTyRGlupheSeSerAlathngluProTyrlleSergly 20

Db 76 AAGCATACCGCTGAGCTTCCTTACGATGCGCTGAGCCCTCCATCTCCAG 135

QY 21 Glnlleasngluile**TyThr 28

Db 136 GAGATCATGACCTTCACACACC 159

Search completed: September 1, 2004, 00:18:26
Job time : 4186 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 31, 2004, 11:39:57 ; Search time 6688 Seconds

(without alignments)
133.951 Million cell updates/sec

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

29: gb_gss2:*

Title: US-09-987-190-2
Sequence: 1 KXSLPDLVPSATREPTISGQINLIXTX 30

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgm2_1/USPTO.spool/US09987190/runat 24082004 161320 24742/app query fasta_1.199
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09987190.@CGN_1_1-3437.@runat 24082004 161320 24742 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

EST:*

1:	em_estda:*
2:	em_esthm:*
3:	em_estim:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hic:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estrom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pin:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rnd:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*

Result
No. Score Match Length DB ID

Result No.	Score	Match	Length	DB	ID	Description
1	141	97.2	862	29	CNS07DTJ	AL440909 T7 end of
2	92	63.4	519	28	AZ929307	AZ929307 479.dif24
3	90	62.1	464	13	B0087025	B0087025 Crt_9 A14
4	87	60.0	379	14	CB935955	CB935955 taad2a04
5	87	60.0	516	12	BP522973	BP522973 BP522973
6	84	57.9	493	13	B0061557	B0061557 Fgr 10 B0
7	84	57.9	669	14	CD425832	CD425832 SAL_14 C1
8	84	57.9	746	13	B0060841	B0060841 Fgr-C_1K
9	83	57.2	231	9	AT319465	AT319465 b2a04nm.f
10	83	57.2	265	9	AT320309	AT320309 C3b05nm.f
11	83	57.2	265	10	AW717655	AW717655 h9g04nm.f
12	83	57.2	267	10	AT318805	AT318805 a2d06nm.f
13	83	57.2	267	10	AW723904	AW723904 f2d01nm.f
14	83	57.2	269	9	AT321638	AT321638 e1d05nm.f
15	83	57.2	336	9	AT320505	AT320505 C5H03nm.f
16	83	57.2	339	9	AT318710	AT318710 a1b10nm.f
17	83	57.2	339	9	AT319577	AT319577 b3g06nm.f
18	83	57.2	340	10	AW715499	AW715499 g4f03nm.f
19	83	57.2	343	10	AW724497	AW724497 f6b04nm.f
20	83	57.2	401	10	AW724781	AW724781 f8b07nm.f
21	83	57.2	429	10	AW715120	AW715120 g2c12nm.f
22	83	57.2	429	10	AW715952	AW715952 g8b12nm.f
23	82	56.6	592	12	BT321452	BT321452 saf11b10
24	82	56.6	689	12	BM266232	BM266232 VA86 CDNA
25	81	55.9	734	14	CD460741	CD460741 Fg09 01k1
26	80	55.2	241	11	AY246752	AY246752 Equus cab
27	80	55.2	466	12	BM167690	BM167690 NKXV_053
28	80	55.2	580	14	CB686471	CB686471 CE8T-01-B
29	80	55.2	675	13	BX255380	BX255380 BX255380
30	80	55.2	682	14	CF883054	CF883054 trico32xk
31	80	55.2	702	14	CF873019	CF873019 trico32xk
32	80	55.2	758	14	CB903040	CB903040 trico32xk
33	80	55.2	767	14	CF392896	CF392896 RTDR3_19
34	80	55.2	828	14	CD467777	CD467777 LeukoS1_6
35	79	54.5	286	14	CA937400	CA937400 s8v18f03
36	79	54.5	306	10	AW733168	AW733168 SK70B06.Y
37	79	54.5	308	14	CA910188	CA910188 PCS01280X
38	79	54.5	419	12	BI498255	BI498255 s8g17h04
39	79	54.5	420	10	AW756619	AW756619 s125a09.Y
40	79	54.5	425	10	BE210200	BE210200 s039h07.Y
41	79	54.5	448	9	AT460811	AT460811 sa69e10.Y
42	79	54.5	448	9	AT460823	AT460823 sa69f10.Y
43	79	54.5	463	9	AW099772	AW099772 sd31c07.Y
44	79	54.5	470	12	BM992237	BM992237 sam57h11
45	79	54.5	493	14	CA910190	CA910190 PCS04450F

ALIGNMENTS

RESULT 1
CNS07DTJ 862 bp DNA linear GSS 08-JUL-2001
LOCUS T7 end of clone BDOAA015F01 of library BDOAA from strain CBS 94 of
DEFINITION Candida tropicalis, genomic survey sequence.
ACCESSION AL440909
VERSION AL440909.1 GI:12224320
KEYWORDS
SOURCE
ORGANISM
Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1 (bases 1 to 862)

AUTHORS
Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brothier, P., Casaregola, S., de Montigny, J., Dujon, B., Durieux, P., Lepingle, A., Llorente, B., Malbertuy, A., Neveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Sautin, M., Tekala, F., Toffano-Nioche, C., Weslowski-Louvel, M., Wincker, P., and Weissbach, J.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL
FEMS Lett. 487 (1), 3-12 (2000)

MEDLINE
20584711

PUBMED
11152876

REFERENCE
2 (bases 1 to 862)

AUTHORS
Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F., and Dujon, B.

TITLE
Genomic exploration of the hemiascomycetous yeasts: 16. *Candida tropicalis*

JOURNAL
FEMS Lett. 487 (1), 91-94 (2000)

MEDLINE
20584726

PUBMED
11152891

REFERENCE
3 (bases 1 to 862)

AUTHORS
Genoscope.

TITLE
Direct Submission

JOURNAL
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : <http://www.genoscope.cns.fr>)

COMMENT
This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
Location/Qualifiers
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/organism="Candida tropicalis"
/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BD0A015F01"
/clone_lib="BD0AA"
/note="end : 77"
/note=">726
/note="Similar to *Saccharomyces cerevisiae* ORF YHR008C [SOD2 ; superoxide dismutase (Mn) precursor, mitochondrial
1"
/evidence=not_experimental

ORIGIN
Alignment Scores:
Pred. No.: 8,296-13 Length: 862
Score: 141.00 Matches: 27
Percent Similarity: 96.43% Conservative: 0
Best Local Similarity: 96.43% Mismatches: 1
Query Match: 97.24% Indels: 0
DB: 29 Gaps: 0

US-09-987-190-2 (1-30) x CNS07DTU (1-862)

QY
1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 130 AAATATAGTTTACCGAATTAGATTGATTTTCTGCTACTGACCATATATTTCTGGA 189

QY
21 GlnIleAsnGluIle***TyrThr 28
DB 190 CAAATTAAATGAATTCATTACT 213

RESULT 2
AZ929307 519 bp DNA linear GSS 01-APR-2001
LOCUS 479.dif24g04.s1 Saccharomyces kluyveri Saccharomyces kluyveri
DEFINITION

ACCESSION
AZ929307
VERSION
AZ929307.1 GI:13500214

KEYWORDS
SOURCE
ORGANISM
Saccharomyces kluyveri

REFERENCE
1 (bases 1 to 519)
Clifton, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.B., Waterston, R.H. and Johnston, M.
Surveying *Saccharomyces* genomes to identify functional elements by comparative DNA sequence analysis
Unpublished (2001)
Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mjgenetics.wustl.edu
Class: random plasmid subclone.

FEATURES
Location/Qualifiers
1..519
/organism="Saccharomyces kluyveri"
/mol_type="genomic DNA"
/strain="NRRL Y-12651 (CBS 3082)"
/db_xref="taxon:4934"
/clone="479.dif24g04.s1"
/clone_lib="Saccharomyces kluyveri"
/note="Random genomic sequence"

ORIGIN
Alignment Scores:
Pred. No.: 5,436-05 Length: 519
Score: 92.00 Matches: 16
Percent Similarity: 82.14% Conservative: 7
Best Local Similarity: 57.14% Mismatches: 5
Query Match: 63.45% Indels: 0
DB: 28 Gaps: 0

US-09-987-190-2 (1-30) x AZ929307 (1-519)

QY
1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
DB 371 AAGGCACTTGCCAGACTTGACCTGCGACTTGGAACCCCAATCTCGGGT 430

QY
21 GlnIleAsnGluIle***TyrThr 28
DB 431 CAAATCAACGAGTTGCACTACTCG 454

RESULT 3
B0087025 464 bp mRNA linear EST 05-APR-2002
LOCUS
DEFINITION
cDNA Clone Cri_9_A14_5', mRNA sequence.
ACCESSION
B0087025
VERSION
B0087025.1 GI:20046226
KEYWORDS
EST
SOURCE
ORGANISM
Ceratopteris richardii
Ceratopteris richardii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Moniliformophyes; Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

REFERENCE
1 (bases 1 to 464)
Chatterjee, A., San Miguel, P., Stout, S.C., Banks, J. and Roux, S.J.
Expressed sequence tags of cDNA clones from a C. richardii library
Unpublished (2000)
Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238

Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Place: Cri_9 row: A column: 14
Seq primer: SP6.

FEATURES
source
Location/Qualifiers

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1..464
/organism="Ceratopteris richardii"
/mol_type="mRNA"
/cultivar="Brogn"
/db_xref="taxon:49495"
/clone="Cri_9_A14"
/tissue_type="Gametophyte"
/cell_type="Spore"
/dev_stage="20 hours after germination initiation"
/clone_lib="Ceratopteris Spore Library"
/note="Vector: PCWSP0RT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."
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ALIGNMENT SCORES:

Pred. No.:	Score:	Length:	Matches:
0.000101	90.00	464	16
Percent Similarity:	81.48%	Conservative:	6
Best Local Similarity:	59.26%	Mismatches:	5
Query Match:	62.07%	Indels:	0
DB:	13	Gaps:	0

US-09-987-190-2 (1-30) x BQ087025 (1-464)

QY 2 TyrsenleuprogileuAepTyrgluPheserAlathrgluProtyrIleserGlyGln 21
154 TACTCTTTACCGAGCTAGCTAGATTATGAGCGCTTACGAGCGCTACATCAGTGGCGAA 213

QY 22 IleasnGlulle**TyrThr 28
214 ATTATGAGCTGCATCAGC 234

RESULT 4
CB935955

LOCUS CB935955 379 bp mRNA linear EST 29-APR-2003
DEFINITION taa42a04.Y2 Hydra EST -111 Hydra magnipapillata cDNA 5' similar to
SW:SDM HUMAN P04179 SUPEROXIDE DISMUTASE [NM], MITOCHONDRIAL
PRECURSOR,, mRNA sequence.

ACCESSION CB935955 GI:30221346
VERSION CB935955
KEYWORDS EST.
SOURCE Hydra magnipapillata
ORGANISM Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
Hydridae; Hydra.

REFERENCE 1 (bases 1 to 379)
Bode,H., Blumberg,B., Steele,R., Widge,P., Gee,L., Nguyen,Q.,
Martinez,D., Kibler,D., Hampton,S., Clifton,S., Pape,D., Marra,M.,
Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
Gibbons,M., Ritzer,B., Bennett,J., Ronko,I., Tsagarelisvili,R.,
Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.

TITLE Wastu Hydra EST Project
JOURNAL Unpublished (2002)
COMMENT Contact: Hans Bode

Wastu Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Bruce Blumberg & Jisong Pang, Univ. of
Calif. Irvine. Library materials provided by Hans Bode & Lydia Gee,
Univ. of Calif., Irvine DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hbode@ucf.edu)
Trace considered overall poor quality

Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

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1..379
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/db_xref="taxon:6085"
/lab_host="DH10B"
/clone_lib="Hydra EST -111"
/note="Vector: pCS22; Site 1: XhoI; Site 2: PstI; a) 1st
strand cDNA was primed with a XhoI oligo (dT) primer (5'
ACTAAGAGGCTCGAG(T)18NN)3'; b) Double-stranded cDNA was
ligated to PstI linker, digested with PstI and XhoI and
cloned into the PstI and XhoI sites of a pCS22 vector,
which is a modified pCS2+ vector. c) The pCS22 vector
contains a T7 promoter site [standard from pluescript] at
the 5' end of the cloning site, and a T3 promoter site
[standard from pluescript] at the 3' end of the cloning
site. d) The ligation mix was transformed into TOP10P
cells (= DH10B cells). e) The cells were grown in SOC =
5% yeast, 20% tryptone, 0.5% NaCl, 10mM MgSO4, 10mM MgCl,
0.2% glucose/liter, (no antibiotic). f) The frequency of
vectors containing inserts is >90% [42 of 42]. g) The
average size of the 42 inserts is 1075 +/- 8501."
```

ALIGNMENT SCORES:

Pred. No.:	Score:	Length:	Matches:
0.000242	87.00	379	17
Percent Similarity:	81.48%	Conservative:	5
Best Local Similarity:	62.96%	Mismatches:	5
Query Match:	60.00%	Indels:	0
DB:	14	Gaps:	0

US-09-987-190-2 (1-30) x CB935955 (1-379)

QY 1 TyrsenleuprogileuAepTyrgluPheserAlathrgluProtyrIleserGly 20
5 AAGCACACTCTTCAGAAATTGGGCTATGATTAATGATTCATGAGACCAACATCAGCGGT 64

QY 21 GlnIleAsnGlulle**Tyr 27
65 CAATATATGAGATCATCAT 85

RESULT 5
BP522973

LOCUS BP522973 516 bp mRNA linear EST 17-SEP-2003
DEFINITION BP522973 Hydra magnipapillata cDNA library Hydra magnipapillata
cDNA clone hmp_21051, mRNA sequence.
BP522973
BP522973.1 GI:34829671

ACCESSION BP522973
VERSION BP522973
KEYWORDS EST.

SOURCE Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
Hydridae; Hydra.

REFERENCE 1 (bases 1 to 516)
Hayakawa,S., Hwang,U.S., Nishimiya-Fujisawa,C., Ogura,A., Ikeo,K.,
Fujisawa,T. and Gojobori,T.

TITLE Hydra EST Project
JOURNAL Unpublished (2003)
COMMENT Contact: Jung Shan Hwang

Center for Information Biology and DNA Data Bank of Japan
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-981-6847 (ex. 6898)
Fax: 81-55-981-6848
Email: jshwang@lab.nig.ac.jp, URL: http://www.cdb.nig.ac.jp.
Location/Qualifiers
1..516
/organism="Hydra magnipapillata"
/mol_type="mRNA"
/strain="105"

/db_xref="taxon:6085"
 /clone="hmp.21051"
 /tissue_type="whole body"
 /dev_stage="adult budding stage"
 /clone_lib="Hydra magnipapillata cDNA library"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	516
Score:	Matches:	17
Percent Similarity:	Conservative:	5
Best Local Similarity:	Mismatches:	5
Query Match:	Indels:	0
DB:	Gaps:	0

US-09-987-190-2 (1-30) x BP522973 (1-516)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 110 AAGCAGCTCTTCCAGATTGGGCTATGAATATATGCAATGGACCAACATCAGCGT 169

QY 21 GnlleAsnGluile**Tyr 27

Db 170 CAATTATGAGATATCATCAT 190

RESULT 6 BU061557 493 bp mRNA linear EST 26-AUG-2002

LOCUS Fgr.10 E01_T3 Nitrogen-starved mycelia Gibberella zeae cDNA, mRNA

DEFINITION sequence.

ACCESSION BU061557 GI:22501846

VERSION EST.

KEYWORDS Gibberella zeae

SOURCE Gibberella zeae

ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 493)

AUTHORS Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.

TITLE Analysis of expressed sequence tags from Gibberella zeae (anamorph Fusarium graminearum)

JOURNAL Fungal Genet. Biol. 38 (2), 187-197 (2003)

MEDLINE 22508120

PUBMED 12620255

COMMENT Contact: Frances Trail

Department of Plant Biology

Michigan State University

East Lansing, MI 48824, USA

Tel: 517 432 2939

Fax: 517 353 1926

Email: trail@msu.edu

Plate: 10 row: E column: 01.

Location/Qualifiers

1. .493

/organism="Gibberella zeae"

/mol_type="mRNA"

/strain="NRRL 31084"

/db_xref="taxon:5518"

/clone_lib="Nitrogen-starved mycelia"

/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	493
Score:	Matches:	15
Percent Similarity:	Conservative:	7
Best Local Similarity:	Mismatches:	6
Query Match:	Indels:	0
DB:	Gaps:	0

US-09-987-190-2 (1-30) x BU061557 (1-493)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 123 AAGCCACTCTCCCGATCTTCCACGATATGCGCTTGGACCCCTACATCTCTGAC 182

QY 21 GnlleAsnGluile**Tyr-Thr 28

Db 183 CAGATCATGAGCTTCACCACTCC 206

RESULT 7

LOCUS CD425832

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

TITLE

JOURNAL

COMMENT

CD425832 669 bp mRNA linear EST 02-JUN-2003

SAI_14.C11.g1.A002 Salicylic acid-treated seedlings Sorghum bicolor

cDNA clone SAI_14.C11.A002 5', mRNA sequence.

CD425832

CD425832.1 GI:31332095

EST.

Sorghum bicolor (sorghum)

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Sorghum.

1 (bases 1 to 669)

Cordonier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,

Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,

Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,

Olaseinde,O., Eastman,A. and Pratt,L.H.

An EST database from Sorghum: salicylic acid-treated seedlings

Unpublished (2003)

Other ESTs: SAI_14.C11.b1.A002

Contact: Cordonier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmp@pratt.uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo. Institute of Medical

Science; plant material and RNA prepared at Texas A & M University;

sequencing done in the Laboratory for Genomics and Bioinformatics;

University of Georgia. Sequence ends have been trimmed to exclude

vector and regions below Phred quality 16. Three-prime sequences

are presented as their reverse complement and have been trimmed to

exclude polyA.

Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).

Location/Qualifiers

1. .669

/organism="Sorghum bicolor"

/mol_type="mRNA"

/cultivar="Brx623"

/db_xref="taxon:4558"

/clone="SAI_14.C11.A002"

/lab_host="DH10B-TI phage-resistant E. coli"

/clone_lib="salicylic acid-treated seedlings"

/note="Vector: pME18S-Fl3; Site_1: XhoI; Site_2: XhoI; The

library was prepared from polyA+ RNA from seedlings grown

in hydroponic culture. At 8 days of age, medium was

supplemented with 1 mM salicylic acid (SA). Roots and

shoots were harvested after 27 and 72 hr and material from

both time points was combined prior to RNA isolation.

Double-stranded cDNA was cloned unidirectionally into

different DraIII sites of the pME18S-Fl3 vector (5-prime

DraIII site is CACTGTGT, 3-prime DraIII site is

CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	669
Score:	Matches:	15
Percent Similarity:	Conservative:	7
Best Local Similarity:	Mismatches:	6
Query Match:	Indels:	0
DB:	Gaps:	0

US-09-987-190-2 (1-30) x BU061557 (1-493)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

US-09-987-190-2 (1-30) x CD425832 (1-669)

QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 299 AAGGCCACCTCCCGCATCTCCCTACGATATGAGCGCTCTTGAGCCTTACATCTCCGCG 358
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 359 CAGATCATGAGAGCTTCACCACTCC 382

RESULT 8
 BU060841 746 bp mRNA linear EST 26-AUG-2002
 LOCUS BU060841
 DEFINITION Fgr-C_1.K18_T3 Carbon-starved mycelia Gibberella zeae cDNA, mRNA
 sequence.
 ACCESSION BU060841 GI:22501130
 VERSION BU060841.1
 KEYWORDS EST.
 SOURCE Gibberella zeae
 ORGANISM Gibberella zeae
 Bkariyota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 REFERENCE 1 Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.
 ANALYSIS of expressed sequence tags from Gibberella zeae (anamorph
 Fusarium graminearum)
 JOURNAL Fungal Genet. Biol. 38 (2), 187-197 (2003)
 MEDLINE 22508120
 PUBMED 12620255

COMMENT
 Contact: Frances Trail
 Department of Plant Biology
 Michigan State University
 East Lansing, MI 48824, USA
 Tel: 517 432 2939
 Fax: 517 353 1926
 Email: trail@msu.edu
 Plate: 1 row: K column: 18.

FEATURES
 source
 Location/Qualifiers
 1..746
 /organism="Gibberella zeae"
 /mol_type="mRNA"
 /strain="NRRL 31084"
 /db_xref="taxon:5518"
 /clone_lib="Carbon-starved mycelia"
 /note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.00183 Length: 746
 Score: 84.00 Matches: 15
 Percent Similarity: 78.57% Conservative: 7
 Best Local Similarity: 53.57% Mismatches: 6
 Query Match: 57.93% Indels: 0
 DB: 13 Gaps: 0

US-09-987-190-2 (1-30) x BU060841 (1-746)
 QY 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20
 Db 134 AAGGCCACCTCCCGCATCTCCCTACGATATGAGCGCTCTTGAGCCTTACATCTCCGCG 193
 QY 21 GlnIleAsnGluIle***TyrThr 28
 Db 194 CAGATCATGAGAGCTTCACCACTCC 217

RESULT 9
 A1319465 231 bp mRNA linear EST 18-DEC-1998
 LOCUS A1319465
 DEFINITION b2a04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
 cDNA clone b2a04nm 5', mRNA sequence.
 ACCESSION A1319465
 VERSION A1319465.1 GI:4035447
 KEYWORDS EST.

SOURCE

Neurospora crassa
 Neurospora crassa
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (bases 1 to 231)
 AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
 TITLE Two Neurospora crassa EST Databases
 JOURNAL Unpublished (1998)
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu

FEATURES
 source
 Location/Qualifiers
 1..231
 /organism="Neurospora crassa"
 /mol_type="mRNA"
 /strain="b2a04nm"
 /db_xref="taxon:5141"
 /clone="b2a04nm"
 /tissue_type="tissue harvested following 22hr growth in dark"
 /clone_lib="Neurospora crassa morning cDNA library"
 /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096-1996.
 5' end of cDNA cloned into XbaI site of pBluescript, 3' end of cDNA cloned into EcoRI site of pBluescript"

ORIGIN
 Alignment Scores:
 Pred. No.: 0.000585 Length: 231
 Score: 83.00 Matches: 15
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 55.56% Mismatches: 6
 Query Match: 57.24% Indels: 0
 DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1319465 (1-231)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 21
 Db 65 TATTCCTCCGACGATACCATATGCTCAATGCTGAGCGCTACATCTCAGCCGAG 124
 QY 22 IleAsnGluIle***TyrThr 28
 Db 125 ATCATGAGAGCTTCACCAAGC 145

RESULT 10
 A1320309 265 bp mRNA linear EST 18-DEC-1998
 LOCUS A1320309
 DEFINITION c3b05nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
 cDNA clone c3b05nm 5', mRNA sequence.
 ACCESSION A1320309
 VERSION A1320309.1 GI:4036291
 KEYWORDS EST.
 SOURCE Neurospora crassa
 ORGANISM Neurospora crassa
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

REFERENCE 1 (bases 1 to 265)
 AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
 TITLE Two Neurospora crassa EST Databases
 JOURNAL Unpublished (1998)
 COMMENT Other_ESTs: c3b05nm.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma

Alignment Scores:

Pred. No.: 0.000706 Length: 267
 Score: 83.00 Matches: 15
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 55.56% Mismatches: 6
 Query Match: 57.24% Indels: 0
 DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1318805 (1-267)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 65 TATTCCTCCGAGCTACCATATGCTCTGAGGCGCTACATCTCAGCCCG 124

QY 22 IleAsnGluLeu**TyrThr 28

Db 125 ATCATGAGCTTCACACAGC 145

RESULT 13
 A1321638
 LOCUS 269 bp mRNA linear EST 18-DEC-1998
 DEFINITION e1d05nm.f1 Neurospora crassa morning CDNA library Neurospora crassa
 CDNA clone e1d05nm 5', mRNA sequence.

ACCESSION A1321638
 VERSION A1321638.1 GI:4037620
 KEYWORDS EST.

SOURCE Neurospora crassa
 ORGANISM Neurospora crassa

REFERENCE
 AUTHORS Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
 TITLE Two Neurospora crassa EST Databases
 JOURNAL Unpublished (1998)

COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu

We anticipate the future release of the CDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: Universal Forward Primer
 High quality sequence stop: 229.

FEATURES
 source location/Qualifiers
 1..267

/organism="Neurospora crassa"
 /mol_type="mRNA"
 /strain="bd, frq7 A"
 /db_xref="taxon:5141"
 /clone="e1d05nm"
 /tissue_type="tissue harvested following 22hr growth in dark"
 /clone_lib="Neurospora crassa morning CDNA library"
 /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:113096, 1996.
 5' end of CDNA cloned into XbaI site of pBluescript; 3' end of CDNA cloned into EcoRI site of pBluescript"

ORIGIN

Alignment Scores:
 Pred. No.: 0.000706 Length: 267
 Score: 83.00 Matches: 15
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 55.56% Mismatches: 6
 Query Match: 57.24% Indels: 0
 DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x A1321638 (1-269)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 65 TATTCCTCCGAGCTACCATATGCTCTGAGGCGCTACATCTCAGCCCG 124

QY 22 IleAsnGluLeu**TyrThr 28

Db 125 ATCATGAGCTTCACACAGC 145

RESULT 14
 A1321638
 LOCUS 269 bp mRNA linear EST 18-DEC-1998
 DEFINITION e1d05nm.f1 Neurospora crassa morning CDNA library Neurospora crassa
 CDNA clone e1d05nm 5', mRNA sequence.

ACCESSION A1321638
 VERSION A1321638.1 GI:4037620
 KEYWORDS EST.

SOURCE Neurospora crassa
 ORGANISM Neurospora crassa

REFERENCE
 AUTHORS Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
 TITLE Two Neurospora crassa EST Databases
 JOURNAL Unpublished (1998)

COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu

We anticipate the future release of the CDNA clones to the Fungal
 Genetics Stock Center
 Seq primer: Universal Forward Primer
 High quality sequence stop: 229.

FEATURES
 source location/Qualifiers
 1..269

/organism="Neurospora crassa"
 /mol_type="mRNA"
 /strain="bd, frq7 A"
 /db_xref="taxon:5141"
 /clone="e1d05nm"
 /tissue_type="tissue harvested following 22hr growth in dark"
 /clone_lib="Neurospora crassa morning CDNA library"
 /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen, D., et al. PNAS 93:113096, 1996.
 5' end of CDNA cloned into XbaI site of pBluescript; 3' end of CDNA cloned into EcoRI site of pBluescript"

ORIGIN

Alignment Scores:
 Pred. No.: 0.000713 Length: 269
 Score: 83.00 Matches: 15
 Percent Similarity: 77.78% Conservative: 6
 Best Local Similarity: 55.56% Mismatches: 6
 Query Match: 57.24% Indels: 0
 DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1321638 (1-269)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

Db 65 TATTCCTCCGAGCTACCATATGCTCTGAGGCGCTACATCTCAGCCCG 124

QY 22 IleAsnGluLeu**TyrThr 28

Db 125 ATCATGAGCTTCACACAGC 145

RESULT 15
 A1320505
 LOCUS 336 bp mRNA linear EST 18-DEC-1998
 DEFINITION c5h03nm.f1 Neurospora crassa morning CDNA library Neurospora crassa
 CDNA clone c5h03nm 5', mRNA sequence.

ACCESSION A1320505

```

VERSION      AI320505.1  GI:4036487
KEYWORDS     EST.
SOURCE       Neurospora crassa
ORGANISM     Neurospora crassa
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 336)
AUTHORS      Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL      Two Neurospora crassa EST Databases
              Unpublished (1998)
COMMENT      Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
              Department of Chemistry and Biochemistry
              Advanced Center for Genome Technology, University of Oklahoma
              620 Parrington Oval, Norman, OK 73019, USA
              Tel: 405 325 4912
              Fax: 405 325 7762
              Email: broe@ou.edu
              We anticipate the future release of the cDNA clones to the Fungal
              Genetics Stock Center
              Seq primer: Universal Forward Primer
              High quality sequence stop: 194.
              Location/Qualifiers
                source
                  1..336
                    /organism="Neurospora crassa"
                    /mol_type="mRNA"
                    /strain="bd, frq7 A"
                    /db_xref="taxon:5141"
                    /clone="csh03nm"
                    /tissue_type="tissue harvested following 22hr growth in
                    dark"
                    /clone_1lb="Neurospora crassa morning cDNA library"
                    /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
                    EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
                    5' end of cDNA cloned into XbaI site of pBluescript; 3'
                    end of cDNA cloned into EcoRI site of pBluescript."

ALIGNMENT SCORES:
Pred. No.:      0.000951      Length:      336
Score:          83.00         Matches:      15
Percent Similarity: 77.78%     Conservative: 6
Best Local Similarity: 55.56%   Mismatches:  6
Query Match:    57.24%         Indels:       0
DB:             9            Gaps:         0

US-09-987-190-2 (1-30) x AI320505 (1-336)
QY      2 TTTCTCTCTCCGAGCTTACCATATGCTCTGAGAGCCCTACATCTCAGCCCG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
        65 TATTCCTTCCGAGCTTACCATATGCTCTGAGAGCCCTACATCTCAGCCCG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
        22 TleAsnGluIle***TyrThr 28
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
        125 ATCATGAGAGCTTACCATCAGC 145

LOCUS       AI318710      339 bp      mRNA      linear      EST 18-DEC-1998
DEFINITION  alb10nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone alb10nm 5', mRNA sequence.
ACCESSION   AI318710
VERSION     AI318710.1  GI:4034645
KEYWORDS    RST.
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 339)
AUTHORS      Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL      Two Neurospora crassa EST Databases
              Unpublished (1998)
COMMENT      Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
              Department of Chemistry and Biochemistry

```

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FEATURES
  source
    1..339
      /organism="Neurospora crassa"
      /mol_type="mRNA"
      /strain="bd, frq7 A"
      /db_xref="taxon:5141"
      /clone="alb10nm"
      /tissue_type="tissue harvested following 22hr growth in
      dark"
      /clone_1lb="Neurospora crassa morning cDNA library"
      /note="Vector: pBluescript SK-; Site 1: XbaI; Site 2:
      EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
      5' end of cDNA cloned into XbaI site of pBluescript; 3'
      end of cDNA cloned into EcoRI site of pBluescript"

ALIGNMENT SCORES:
Pred. No.:      0.000962      Length:      339
Score:          83.00         Matches:      15
Percent Similarity: 77.78%     Conservative: 6
Best Local Similarity: 55.56%   Mismatches:  6
Query Match:    57.24%         Indels:       0
DB:             9            Gaps:         0

US-09-987-190-2 (1-30) x AI318710 (1-339)
QY      2 TTTCTCTCTCCGAGCTTACCATATGCTCTGAGAGCCCTACATCTCAGCCCG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
        65 TATTCCTTCCGAGCTTACCATATGCTCTGAGAGCCCTACATCTCAGCCCG 124
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
        22 TleAsnGluIle***TyrThr 28
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
        :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
        125 ATCATGAGAGCTTACCATCAGC 145

LOCUS       AI319577      339 bp      mRNA      linear      EST 18-DEC-1998
DEFINITION  b3g06nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
            cDNA clone b3g06nm 5', mRNA sequence.
ACCESSION   AI319577
VERSION     AI319577.1  GI:4035559
KEYWORDS    EST.
SOURCE      Neurospora crassa
ORGANISM    Neurospora crassa
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
              Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE    1 (bases 1 to 339)
AUTHORS      Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL      Two Neurospora crassa EST Databases
              Unpublished (1998)
COMMENT      Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
              Department of Chemistry and Biochemistry
              Advanced Center for Genome Technology, University of Oklahoma
              620 Parrington Oval, Norman, OK 73019, USA
              Tel: 405 325 4912
              Fax: 405 325 7762
              Email: broe@ou.edu
              We anticipate the future release of the cDNA clones to the Fungal
              Genetics Stock Center
              Seq primer: Universal Forward Primer
              High quality sequence stop: 314.
              Location/Qualifiers
                source
                  1..339
                    /organism="Neurospora crassa"

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ORIGIN

/mol_type="mRNA"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="b3g06m"
/tissue="tissue harvested following 22hr growth in dark"
/clone_1ib="Neurospora crassa morning cDNA library"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"

Alignment Scores:
Pred. No.: 0.000962 Length: 339
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 9 Gaps: 0

US-09-987-190-2 (1-30) x A1319577 (1-339)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||
65 TATTCCTTCGCGAGCTACCATATGCTCAATGCTCTGGAGCCCTACATCTCAGCCGAG 124
|||||
QY 22 IleAsnGluIle***TyrThr 28
|||||
DB 125 ATCATGAGCTTCACCAACAGC 145

RESULT 18
AW715499 340 bp mRNA linear EST 19-APR-2000
LOCUS g4f03nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
DEFINITION cDNA clone g4f03nm 5', mRNA sequence.
ACCESSION AW715499
VERSION AW715499.1 GI:7604640
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa

REFERENCE 1 (bases 1 to 340)
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE Two Neurospora crassa EST Databases
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 315.
Location/Qualifiers
1..340
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="g4f03nm"
/tissue_type="tissue harvested following 22hr growth in dark"
/clone_1ib="Neurospora crassa morning cDNA library"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 0.000966 Length: 340
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW715499 (1-340)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||||
65 TATTCCTTCGCGAGCTACCATATGCTCAATGCTCTGGAGCCCTACATCTCAGCCGAG 124
|||||
QY 22 IleAsnGluIle***TyrThr 28
|||||
DB 125 ATCATGAGCTTCACCAACAGC 145

RESULT 19
AW724497 343 bp mRNA linear EST 19-APR-2000
LOCUS f6b04nm.f1 Neurospora crassa morning cDNA library Neurospora crassa
DEFINITION cDNA clone f6b04nm 5', mRNA sequence.
ACCESSION AW724497
VERSION AW724497.1 GI:7619057
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa

REFERENCE 1 (bases 1 to 343)
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
AUTHORS Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
TITLE Two Neurospora crassa EST Databases
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 324.
Location/Qualifiers
1..343
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="f6b04nm"
/tissue_type="tissue harvested following 22hr growth in dark"
/clone_1ib="Neurospora crassa morning cDNA library"
/note="Vector: pBluescript SK-; Site 1: XbaI; Site 2: EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 0.000977 Length: 343
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AW724497 (1-343)

QY 2 TySerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21

```

Db      65 TATTCCTCCGAGCTACCATATGCTTACATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
Db      125 ATCATGAGCTTCACACAGC 145

RESULT 20
AM724781
LOCUS   401 bp mRNA linear EST 19-APR-2000
DEFINITION
CDNA clone FB07nm.5', mRNA sequence.
ACCESSION
AM724781
VERSION
AM724781.1 GI:7619341
KEYWORDS
EST.
SOURCE  Neurospora crassa
        Neurospora crassa
        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
        Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
1 (bases 1 to 401)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL
Two Neurospora crassa EST Databases
Unpublished (1998)
COMMENT
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 394.
Location/Qualifiers
1.401
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="FB07nm"
/tissue_type="tissue harvested following 22hr growth in
dark"
/clone_lib="Neurospora crassa morning CDNA library"
/note="Vector: pBluescript SK-, Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of CDNA cloned into XbaI site of pBluescript; 3'
end of CDNA cloned into EcoRI site of pBluescript."

ORIGIN
Alignment Scores:
Pred. No.: 0.0012 Length: 401
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AM724781 (1-401)

QY      2 TysrleuprogluenuaspTyrGluPheseralathrGluProTyrIleserglyin 21
Db      65 TATTCCTCCGAGCTACCATATGCTTACATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
Db      125 ATCATGAGCTTCACACAGC 145

RESULT 21
AM715120
LOCUS   429 bp mRNA linear EST 19-APR-2000
DEFINITION
CDNA clone g2c12nm.5', mRNA sequence.
ACCESSION
AM715120
VERSION
AM715120.1 GI:7604309
KEYWORDS
EST.
SOURCE  Neurospora crassa
        Neurospora crassa
        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
        Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
1 (bases 1 to 429)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL
Two Neurospora crassa EST Databases
Unpublished (1998)
COMMENT
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 336.
Location/Qualifiers
1.429
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="g2c12nm"
/tissue_type="tissue harvested following 22hr growth in
dark"
/clone_lib="Neurospora crassa morning CDNA library"
/note="Vector: pBluescript SK-, Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of CDNA cloned into XbaI site of pBluescript; 3'
end of CDNA cloned into EcoRI site of pBluescript."

ORIGIN
Alignment Scores:
Pred. No.: 0.00131 Length: 429
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AM715120 (1-429)

QY      2 TysrleuprogluenuaspTyrGluPheseralathrGluProTyrIleserglyin 21
Db      65 TATTCCTCCGAGCTACCATATGCTTACATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
Db      125 ATCATGAGCTTCACACAGC 145

RESULT 22
AM715952
LOCUS   429 bp mRNA linear EST 19-APR-2000
DEFINITION
CDNA clone g8b12nm.5', mRNA sequence.
ACCESSION
AM715952
VERSION
AM715952.1 GI:7605157
KEYWORDS
EST.
SOURCE  Neurospora crassa
        Neurospora crassa
        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
        Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
1 (bases 1 to 429)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL
Two Neurospora crassa EST Databases
Unpublished (1998)
COMMENT
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

```

```

ACCESSION
AM715120
VERSION
AM715120.1 GI:7604309
KEYWORDS
EST.
SOURCE  Neurospora crassa
        Neurospora crassa
        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
        Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
1 (bases 1 to 429)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL
Two Neurospora crassa EST Databases
Unpublished (1998)
COMMENT
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 336.
Location/Qualifiers
1.429
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="bd, frq7 A"
/db_xref="taxon:5141"
/clone="g2c12nm"
/tissue_type="tissue harvested following 22hr growth in
dark"
/clone_lib="Neurospora crassa morning CDNA library"
/note="Vector: pBluescript SK-, Site 1: XbaI; Site 2:
EcoRI; See: Bell-Pedersen,D., et al. PNAS 93:13096,1996.
5' end of CDNA cloned into XbaI site of pBluescript; 3'
end of CDNA cloned into EcoRI site of pBluescript."

ORIGIN
Alignment Scores:
Pred. No.: 0.00131 Length: 429
Score: 83.00 Matches: 15
Percent Similarity: 77.78% Conservative: 6
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 57.24% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x AM715120 (1-429)

QY      2 TysrleuprogluenuaspTyrGluPheseralathrGluProTyrIleserglyin 21
Db      65 TATTCCTCCGAGCTACCATATGCTTACATGCTCTGAGCCCTACATCTCAGCCAG 124
QY      22 Tleasngluile***TyrThr 28
Db      125 ATCATGAGCTTCACACAGC 145

RESULT 22
AM715952
LOCUS   429 bp mRNA linear EST 19-APR-2000
DEFINITION
CDNA clone g8b12nm.5', mRNA sequence.
ACCESSION
AM715952
VERSION
AM715952.1 GI:7605157
KEYWORDS
EST.
SOURCE  Neurospora crassa
        Neurospora crassa
        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
        Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE
1 (bases 1 to 429)
AUTHORS
Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
JOURNAL
Two Neurospora crassa EST Databases
Unpublished (1998)
COMMENT
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

```


	COMMENT
Contact:	Duplessis S
UMR 1136 INRA/UHP Interactions Arbres/Micro-Organismes	
INRA	
Centre INRA de Nancy, 54280 Champenoux, France	
Tel.: + 33 383 39 40 13	
Fax: + 33 383 39 40 69	
Email: duplessis@nancy.inra.fr	
Insert Length: 689 Std Error: 0.00	
Seq primer: T3	
POLYA=No.	
FEATURES	
Source	
Location/Qualifiers	
1..689	
/organism="Tuber borchii"	
/mol_type="mRNA"	
/db_xref="taxon:42251"	
/tissue_type="mycelium"	
/dev_stage="vegetative hyphae"	
/clone_lib="cDNA library of Tuber borchii vegetative mycelium grown on PDA agar medium"	
/note="Organ: mycelium; Vector: pBK-CMV phagemid; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from total RNA of Tuber borchii mycelium grown on PDA agar medium using the UniZapXR cDNA library System Construction kit (Stratagene, USA) according to the manufacturer's instructions. UniZapXR clones were converted to pBK-CMV phagemid clones using E. coli BM25.8 as the bacterial host"	
Alignment Scores:	
Pred. No.:	0.00353
Score:	82.00
Percent Similarity:	75.00%
Best Local Similarity:	53.57%
Query Match:	56.55%
DB:	12
Gaps:	0
US-09-987-190-2 (1-30) x BM266232 (1-689)	
QY	1 LysTyrSerLeuProGlnLeuAspTyrGlnPheSerAlaThrGluProTyrTlleSerGly 20
Db	404 AAGTTATCTCTCCGGGATGCGGTATGCATTATGATGACGCTAACCCTTCATCTCCGCC 463
QY	21 GlnIleAsngluIle***TyrThr 28
Db	464 CAATATGCAAATCCACCATTC 487
RESULT 25	
CD460741	734 bp mRNA linear EST 03-JUN-2003
LOCUS	Fg09_01k18_A Fg09 AAF_C EOORC Fusarium graminearum simple_substrate
DEFINITION	Gibberella zeae cDNA clone Fg09_01k18, mRNA sequence.
ACCESSION	CD460741
VERSION	CD460741.1 GI:31375481
KEYWORDS	EST.
SOURCE	Gibberella zeae
ORGANISM	Gibberella zeae Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE	1 (bases 1 to 734) Watson,R.J., Hey's,R., Courroux,P., De Moors,A., Harris,L.J., Hatori,J., Iacoxix,C., Masotti,M., Ouellet,T., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A. A cDNA library prepared from Fusarium graminearum grown on a simple substrate
AUTHORS	Unpublished (2003)
JOURNAL	Contact: Watson, Robert.J. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6, CANADA Tel.: (613) 759-1655 Fax: (613) 759-1701
COMMENT	

[illegible]

ORIGIN	Alignment Scores:	Pred. No.:	0.00455	Length:	466
Score:	80.00	Matches:	15		
Percent Similarity:	76.92%	Conservative:	5		
Best Local Similarity:	57.69%	Mismatches:	6		
Query Match:	55.17%	Indels:	0		
DB:	12	Gaps:	0		
US-09-987-190-2 (1-30) x BM67690 (1-466)					
Qy	2 TyserleupfpgiuleuapryrGluPheserAlathrshupProYrIleserGIyGln 21				
Db	204 TTGATGTACCGGAGCTTCATACGAAATACAGCGGCATTGACACGGTTATTATGCGTACG 263				
Qy	22 TLeansnltule***Tyr 27				
Db	264 ATTATGAGCCTTGACACGAC 281				
RESULT 28					
LOCUS	CB686471	580 bp	mRNA	linear	EST 04-SEP-2003
DEFINITION	CEST-01-B-09 Mixed source, strain EP15 and EP15 infected with hypovirus CHV1-EP713 Cryphonectria parasitica cDNA clone EP155, EP155-CHV1-EP713 5-prime, mRNA sequence.				
ACCESSION	CB686471				
VERSION	CB686471.1	GI:34447340			
KEYWORDS	EST.				
SOURCE	Cryphonectria parasitica				
ORGANISM	Cryphonectria parasitica				
	Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Diaporthales; Valsaceae; Cryphonectria-Endothia complex; Cryphonectria.				
REFERENCE	1 (bases 1 to 580)				
AUTHORS	Dawe,A.L., McManis,V.C., Panglao,M., Kasahara,S., Chen,B. and Nuss,D.L.				
TITLE	An ordered collection of expressed sequences from Cryphonectria parasitica and evidence of genomic microsynteny with Neurospora crassa and Magnaporthe grisea				
JOURNAL	Microbiology 149 (9), 2373-2384 (2003)				
MEDLINE	22830414				
PUBMED	12949163				
COMMENT	Contact: Dawe AL, Nuss DL Center for Biosystems Research University of Maryland Biotechnology Institute 5115 Plant Sciences Building, College Park, MD 20742, USA Tel: 301-405-7661 or 5111 Fax: 301-314-9075 Email: dawe@umbl.umd.edu Cryphonectria parasitica EST derived from mixed samples of cDNA from wild-type (strain EP155) and hypovirus-infected cultures. Seq primer: M13-reverse. Location/Qualifiers 1. 580 /organism="Cryphonectria parasitica" /mol_type="mRNA" /strain="EP155" /db_xref="ATCC (inhost):38755 and 52571" /db_xref="taxon:5116" /clone_1b="Mixed source, strain EP155 and EP155 infected with hypovirus CHV1-EP713" /note="Cryphonectria parasitica EST derived from mixed samples of cDNA from wild-type (strain EP155) and hypovirus-infected cultures"				
FEATURES					
source					
ORIGIN					

University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source
1..767
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="FDR3_19_A06_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Lobliolly pine roots recovering from drought DR3"
/note="vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from lobliolly pine (Pinus taeda) roots recovering from drought. Water was withheld from ramet clones until predawn needle water potential reached -1.75 MPa. Plants were well watered on day 7 and allowed to recover for 2 days, at which time roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:
Pred. No.: 0.00869 Length: 767
Score: 80.00 Matches: 15
Percent Similarity: 76.92% Conservative: 5
Best Local Similarity: 57.69% Mismatches: 6
Query Match: 55.17% Indels: 0
DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x CF392896 (1-767)

Qy 2 TySeriLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyCln 21

Db 204 TTTAGTTTACCGAGCTTCATACGATACAGCGCATGGAAACCGTTATTAGTGGTGG 263

Qy 22 IleAsnGluIle***Tyr 27

Db 264 ATTATGAGCTGCACACC 281

RESULT 34

CD467777

LOCUS

DEFINITION LeukoS1_6_G06.g1_A023 Stimulated peripheral blood leukocytes S1

CD467777 Equus caballus cDNA clone LeukoS1_6_G06_A023 5', mRNA sequence.

ACCESSION CD467777.1 GI:31389045

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other ESTs: LeukoS1_6_G06.b1_A023
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical

Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).

FEATURES

source
1..828
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Belgian draft"
/db_xref="taxon:9796"
/clone="LeukoS1_6_G06_A023"
/sex="female"
/tissue_type="blood"
/cell_type="leukocytes"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Stimulated peripheral blood leukocytes S1"
/note="Organ: circulatory system; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from equine peripheral blood leukocytes isolated from a healthy adult horse. The leukocytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 IPS. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:
Pred. No.: 0.0096 Length: 828
Score: 80.00 Matches: 13
Percent Similarity: 78.57% Conservative: 9
Best Local Similarity: 46.43% Mismatches: 6
Query Match: 55.17% Indels: 0
DB: 14 Gaps: 0

US-09-987-190-2 (1-30) x CD467777 (1-828)

Qy 1 LysTyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGly 20

Db 128 AAGCACAGCTCCCGCAGTTCAGTATGCGCTCTGGAGCCCTACATCAACGCC 187

Qy 21 GlnIleAsnGluIle***TyrThr 28

Db 188 CAGATCATGAGCTGCACACAGC 211

RESULT 35

CA937400

LOCUS

DEFINITION

CA937400

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA937400 286 bp mRNA linear EST 30-DEC-2002
sav18f03.y1 Gm-cl048 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl048-6005 5' similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE
[MN], MITOCHONDRIAL PRECURSOR i, mRNA sequence.
CA937400
CA937400.1 GI:27425880
EST.
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 286)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 242.

FEATURES

source

```
1. .286
   Location/Qualifiers
     .286
       /organism="Glycine max"
       /mol_type="mRNA"
       /db_xref="taxon:3847"
       /clone="SOYBEAN CLONE ID: Gm-cl048-6005"
       /tissue_type="whole seedlings of greenhouse grown plants"
       /dev_stage="1 week old"
       /lab_host="DH10B"
       /clone_lib="Gm-cl048"
       /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 1 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."
```

ORIGIN

Alignment Scores:

```
Pred. No.: 0.00354 Length: 286
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 14 Gaps: 0
```

US-09-987-190-2 (1-30) x CA937400 (1-286)

```
QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 TACACGCTCCCGATCTGGATTACGACTATGCGCTCTGGAGCCGCCATCAGCGGGAA 176
QY 22 IleAsnGluIle***Tyr 27
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 ATCATGCAGCTGCACCAC 194
```

RESULT 36

AW733168

LOCUS

DEFINITION

AW733168 306 bp mRNA linear EST 03-DEC-2001
Gm-cl016-9492 5', similar to SW:SODM_PEA P27084 SUPEROXIDE DISMUTASE
[MN] PRECURSOR ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 306)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.

TITLE

JOURNAL

COMMENT

Public Soybean EST Project
Published (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1240 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 305.

FEATURES

source

```
1. .306
   Location/Qualifiers
     .306
       /organism="Glycine max"
       /mol_type="mRNA"
       /db_xref="taxon:3847"
       /clone="GENOME SYSTEMS CLONE ID: Gm-cl016-9492"
       /tissue_type="immature flowers of field grown plants"
       /lab_host="Xl10-Gold"
       /clone_lib="Gm-cl016"
       /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into Xl10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelting."
```

ORIGIN

Alignment Scores:

```
Pred. No.: 0.00386 Length: 306
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 10 Gaps: 0
```

US-09-987-190-2 (1-30) x AW733168 (1-306)

```
QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 160 TACACGCTCCCGATCTGGATTACGACTATGCGCTCTGGAGCCGCCATCAGCGGGAA 219
QY 22 IleAsnGluIle***Tyr 27
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 ATCATGCAGCTGCACCAC 237
```

RESULT 37

CA910188

LOCUS

DEFINITION

CA910188 308 bp mRNA linear EST 27-DEC-2002
PCS01280X5F Scarlet Runner Bean Suspensor Region TripLex2 Phaseolus
coccineus cDNA 5', similar to Superoxide dismutase, mitochondrial
precursor, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

CA910188.1 GI:27397180
EST.


```

Pred. No.: 0.00581 Length: 419
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 12 Gaps: 0

US-09-987-190-2 (1-30) x BI498255 (1-419)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 144 TACAGCTCCCGATCTGGATTACGATATGGCGCTCTGGAGCCAGCATCAGCGGTGAA 203
QY 22 IleAsnGluIle***Tyr 27
Db 204 ATCATGCAGTCGCCAC 221

RESULT 39
AW756619 420 bp mRNA linear EST 03-DEC-2001
DEFINITION s125a09.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
[MN] PRECURSOR ;, mRNA sequence.
ACCESSION AW756619.1 GI:7685971
VERSION AW756619.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 420)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 417.
Location/Qualifiers
1. 420
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon.3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl027-2321"
/tissue_type="cotyledons of 3- and 7-day-old Williams
seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl027"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels with distilled
water. The cotyledons were flash-frozen in liquid
nitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthesis Kit (catalog number 200401) was used to
synthesize the cDNA. First- stranded synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor
nucleotide (V=A, C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18] to anchor
the primer at the 5' end of the poly(A) tract. After
second- strand synthesis, the cDNA ends were filled in
with cloned pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500 bp cutoff
using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript(tm) II XR Predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). 97% of the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=30). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

ORIGIN
Alignment Scores:
Pred. No.: 0.00582 Length: 420
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 12 Gaps: 0

US-09-987-190-2 (1-30) x AW756619 (1-420)

QY 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 136 TACAGCTCCCGATCTGGATTACGATATGGCGCTCTGGAGCCAGCATCAGCGGTGAA 195
QY 22 IleAsnGluIle***Tyr 27
Db 196 ATCATGCAGTCGCCAC 213

RESULT 40
AW756619 425 bp mRNA linear EST 04-DEC-2001
DEFINITION s039n07.y1 Gm-cl039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
[MN] PRECURSOR ;, mRNA sequence.
ACCESSION BE210200.1 GI:8826470
VERSION BE210200.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 425)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 417.
Location/Qualifiers
1. 425
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon.3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-374"
/tissue_type="cotyledons of 3- and 7-day-old Williams
seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl039"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old Williams seedlings
which were propagated on paper towels with distilled
water. The cotyledons were flash-frozen in liquid
nitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthesis Kit (catalog number 200401) was used to
synthesize the cDNA. First- stranded synthesis was
performed with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor
nucleotide (V=A, C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18] to anchor
the primer at the 5' end of the poly(A) tract. After
second- strand synthesis, the cDNA ends were filled in
with cloned pfu DNA, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500 bp cutoff
using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pBluescript(tm) II XR Predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). 97% of the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=30). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

```

call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 2110 Std Error: 0.00
High quality sequence stop: 424.
Location/Qualifiers
1. .425
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl039-374"
/tissue_type="whole seedling without cotyledons"
/lab_host="DH10B"
/clone_lib="Gm-cl039"
/note="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker."

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 0.00591 Length: 425
Score: 79.00 Matches: 13
Percent Similarity: 80.77% Conservative: 8
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 54.48% Indels: 0
DB: 10 Gaps: 0

US-09-987-190-2 (1-30) x BE210200 (1-425)

Qy 2 TyrSerLeuProGluLeuAspTyrGluPheSerAlaThrGluProTyrIleSerGlyGln 21
Db 159 TACACGCTCCCGATCTGTGATTACGACTATGGCGCTCTGGAGCCGCCATCAGCGGTGAA 218
Qy 22 IleAsnGluIle***Tyr 27
Db 219 ATCATGAGCTGCACAC 236

Search completed: August 31, 2004, 21:57:15
Job time : 6697 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 22:47:41 ; Search time 122 Seconds
(without alignments)
69.479 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYEFSGATEPIYISQINEIXYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	2	Aaw53252 Candida a
2	101	69.7	207	5	Aaol15875 Mycobacte
3	100	69.0	233	5	Abb05612 S. cerevi
4	94	64.8	207	5	Aaol15874 Mycobacte
5	79	54.5	30	2	Aaw29762 Malassezi
6	79	54.5	224	2	Aaw29771 Malassezi
7	77	53.1	200	4	Aaoo0514 C. melass
8	77	53.1	200	4	Aag92973 C glutani
9	74	51.0	95	5	Aae24641 Human MAS
10	74	51.0	101	3	Aag02172 Human sec
11	74	51.0	155	4	Aau30130 Novel hum
12	74	51.0	183	2	Aay29656 Human man
13	74	51.0	198	1	Aap80603 Sequence
14	74	51.0	198	1	Aap80602 Sequence
15	74	51.0	198	2	Aar75191 Human man
16	74	51.0	198	2	Aar75192 Human man
17	74	51.0	198	3	Aay55846 Human man
18	74	51.0	199	2	Aar20015 Mn-SOD (I
19	74	51.0	199	2	Aar60359 MnSOD N-t
20	74	51.0	222	1	Aap71701 Recombina
21	74	51.0	222	2	Aar44801 MnSOD cDN
22	74	51.0	222	2	Aar61337 Human man
23	74	51.0	222	2	Aar75193 Human man
24	74	51.0	222	2	Aar90713 Human man
25	74	51.0	222	2	Aaw00018 Human man

26	74	51.0	222	2	Aaw00453 Human man
27	74	51.0	222	2	Aaw96317 Human man
28	74	51.0	222	2	Aaw82446 Human mso
29	74	51.0	222	2	Aaw98177 Human man
30	74	51.0	222	2	Aaw98175 Human man
31	74	51.0	222	2	Aaw98172 Human man
32	74	51.0	222	2	Aaw98171 Human man
33	74	51.0	222	2	Aaw98170 Human nat
34	74	51.0	222	2	Aaw98174 Human man
35	74	51.0	222	2	Aaw98169 Human nat
36	74	51.0	222	2	Aaw98173 Human nat
37	74	51.0	222	2	Aaw98176 Human man
38	74	51.0	222	3	AAB08206 A modifie
39	74	51.0	222	3	AAB08205 Q143N mod
40	74	51.0	222	3	AAB08204 Amino aci
41	74	51.0	222	5	ABB79798 Human man
42	74	51.0	222	5	ABB07330 Human man
43	74	51.0	222	7	ADD45869 Rat Prote
44	74	51.0	223	1	AAP80551 Human man
45	74	51.0	226	3	AAY55849 Human man

ALIGNMENTS

RESULT 1
AAW53252
ID AAW53252 standard; protein; 30 AA.
XX AC
XX AAW53252;
XX AC
DT 30-JUL-1998 (first entry)
XX
DE Candida albicans allergen - antigenic protein SEQ ID NO:2.
XX
KW Candida albicans; vaccine; allergen; antigenic protein; fungal antigen;
KW immune response; infection; insoluble.
XX
OS Candida albicans.
XX
FH Key Location/Qualifiers
FT Misc-difference 26 /note= "any amino acid"
FT Misc-difference 23 /note= "any amino acid"
FT Misc-difference 30 /note= "any amino acid"
XX
XX WO9809990-A1.
XX
PD 12-MAR-1998.
XX
PF 29-AUG-1997; 97WO-JP003041.
XX
PR 04-SEP-1996; 96JP-00255400.
PR 31-MAR-1997; 97JP-00099775.
XX
XX (TAKI) TAKARA SHUZO CO LTD.
XX
XX Takesako K, Mizutani S, Endo M, Kato I;
XX WPI; 1998-193553/17.
XX
XX Fungal antigens comprising insoluble fraction of fungal cells - useful
XX for, e.g. stimulating immune response and treatment and diagnosis of
XX fungal infection(s).
XX
XX Claim 26; Page 75; 108pp; Japanese.
XX
XX The present sequence represents an active vaccine component or allergen
XX derived from Candida albicans, which is an antigenic protein. The present
XX invention describes fungal antigens, comprising the insoluble fraction of
XX fungal cells having completely/partially removed cell walls. Also

DT 16-JAN-2003 (first entry)
XX Mycobacterium tuberculosis soda protein.
DE
XX
XX Mycobacterium detection method; soda; sod; pncA.
KW
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO200274991-A2.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 20-MAR-2002; 2002WO-GB001308.
PF
XX
XX 20-MAR-2001; 2001GB-00006949.
PR
XX
XX (NORC-) NORCHIP AS.
PA
XX (ALLA/) ALLARD S J.
PI
XX Karlsen F;
DR
XX WPI; 2002-750564/B1.
XX N-PSDB; ABT12954.
DR
XX
XX Detecting the presence of Mycobacterium tuberculosis in a test sample,
PT comprises inducing mRNA expression of Mycobacterium tuberculosis and
PT detecting the induced mRNA.
XX
XX Example 5; Page 56-57; 70pp; English.
PS
XX
XX The invention comprises a method for detecting the presence of a micro-
CC organism (particularly Mycobacterium tuberculosis) in a test sample. The
CC method of the invention comprises exposing the test sample to an inducer
CC that is capable of inducing the expression of at least one gene in the
CC micro-organism and then testing for the presence of mRNA from this gene.
CC The method of the invention is useful for detecting an mRNA that is
CC expressed in a species of Mycobacterium (e.g. Mycobacterium
CC tuberculosis). The present amino acid sequence represents a Mycobacterium
CC protein which was used in an example of the invention
XX
XX Sequence 207 AA;
SQ
Query Match 64.8%; Score 94; DB 5; Length 207;
Best Local Similarity 53.6%; Pred. No. 5.1e-07;
Matches 15; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 1 KYSLPELDYFSGATEPYISQINEIXYT 28
Db 3 EYTLPLDWDYGALEPHISQINELHHS 30
RESULT 5
AAW29762
ID AAW29762 standard; peptide; 30 AA.
XX
XX
XX AAW29762;
AC
XX
XX 27-AUG-2003 (revised)
DT 20-FEB-1998 (first entry)
XX
XX Malassezia fungus MF-4 antigenic peptide.
DE
XX
XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
KW allergy; antigen.
XX
XX Malassezia.
OS
XX WO9721817-A1.
PN
XX
XX 19-JUN-1997.
PD
XX
XX 10-DEC-1996; 96WO-JP003602.
PF
XX
XX 12-DEC-1995; 95JP-00346627.
PR 05-SEP-1996; 96JP-00257612.
XX 05-SEP-1996; 96JP-00257613.
PR
XX
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI Akiyama K, Yasueda H, Yamaguchi H;
XX
XX WPI; 1997-332788/30.
PN
XX
XX 19-JUN-1997.
PD
XX
XX 10-DEC-1996; 96WO-JP003602.
PF
XX
XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
PT present in patients with Malassezia allergies, useful for diagnosis,
PT treatment and prevention of such conditions.

PR 12-DEC-1995; 95JP-00346627.
PR 05-SEP-1996; 96JP-00257612.
PR 05-SEP-1996; 96JP-00257613.
XX
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI Akiyama K, Yasueda H, Yamaguchi H;
XX
XX WPI; 1997-332788/30.
PN
XX
XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
PT present in patients with Malassezia allergies, useful for diagnosis,
PT treatment and prevention of such conditions.
XX
XX Claim 8; Page 113; 162pp; Japanese.
PS
XX
XX The present sequence represents a specifically claimed antigenic peptide
CC isolated from the fungus Malassezia. The antigenic peptide can bind to
CC IgE antibodies present in patients with allergic conditions. Antigenic
CC proteins, peptides and nucleic acids from the fungus Malassezia can be
CC used in the diagnosis, treatment and prevention of allergic conditions
CC due to Malassezia organisms (such as M.furur, M. sympodialis and
CC M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 30 AA;
SQ
Query Match 54.5%; Score 79; DB 2; Length 30;
Best Local Similarity 55.6%; Pred. No. 1.4e-05;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 KYSLPELDYFSGATEPYISQINEIXY 27
Db 1 KYTLPLPDYDYGALPAISGEIMETHY 27
RESULT 6
AAW29771
ID AAW29771 standard; protein; 224 AA.
XX
XX AAW29771;
AC
XX
XX 27-AUG-2003 (revised)
DT 23-FEB-1998 (first entry)
XX
XX Malassezia fungus MF-4 antigenic protein.
DE
XX
XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
KW allergy; antigen.
XX
XX Malassezia.
OS
XX WO9721817-A1.
PN
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XX 19-JUN-1997.
PD
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XX 10-DEC-1996; 96WO-JP003602.
PF
XX
XX 12-DEC-1995; 95JP-00346627.
PR 05-SEP-1996; 96JP-00257612.
XX 05-SEP-1996; 96JP-00257613.
PR
XX
XX (TAKI) TAKARA SHUZO CO LTD.
PA
XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI Akiyama K, Yasueda H, Yamaguchi H;
XX
XX WPI; 1997-332788/30.
PN
XX
XX N-PSDB; AAT85877.
PD
XX
XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
PT present in patients with Malassezia allergies, useful for diagnosis,
PT treatment and prevention of such conditions.

XX Claim 38; Page 85-86; 162pp; Japanese.

XX The present sequence represents a specifically claimed antigenic protein isolated from the fungus *Malassezia*. The antigenic protein can bind to IgE antibodies present in patients with allergic conditions. Antigenic proteins, peptides and nucleic acids from the fungus *Malassezia* can be used in the diagnosis, treatment and prevention of allergic conditions due to *Malassezia* organisms (such as *M. furfur*, *M. sympodialis* and *M. pachydermatitis*). (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 224 AA;

Query Match 54.5%; Score 79; DB 2; Length 224;
Best Local Similarity 55.6%; Pred. No. 0.00017;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXY 27
DB 25 KYTLPLPDYDGALEPAISGEIMETHY 51

RESULT 7
AAU00514
ID AAU00514 standard; protein; 200 AA.
XX AC AAU00514;
XX 09-MAY-2001 (first entry)
XX C. melassecola superoxide dismutase.
XX Superoxide dismutase; sod; coryneform microorganism; metabolite; vitamin;
XX D-pantothenic acid; L-lysine; amplification; animal nutrition.
XX Corynebacterium melassecola.
XX EP1077261-A2.
XX 21-FEB-2001.
XX 02-AUG-2000; 2000EP-00116669.
XX 13-AUG-1999; 99US-00373731.
XX (DEGS) DEGUSSA-HUELS AG.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX Merkamm M, Guyonvarch A, Marx A;
XX WPI; 2001-212718/22.
XX N-PSDB; AAS00520.
XX New DNA encoding superoxidase dismutase of *Corynebacterium*, useful for
XX producing transformants with increased production of metabolites,
XX particularly lysine.
XX Claim 3; Page 14-15; 19pp; English.

XX The sequence represents *Corynebacterium melassecola* superoxide dismutase (sod) polypeptide. *Coryneform* microorganisms may be transformed with a sod DNA sequence and the sod gene can be amplified. Sod is then often overexpressed in *coryneform* bacteria. *Coryneforms* that overexpress sod are used for production of metabolites, particularly nucleotides, vitamins and amino acids, especially D-pantothenic acid or, specifically, L-lysine. These metabolites are useful in human or animal nutrition and as pharmaceuticals. Overexpression of sod in *coryneforms* increases the yield of particular metabolites

XX Sequence 200 AA;

Query Match 53.1%; Score 77; DB 4; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.00032;

XX Query Match 53.1%; Score 77; DB 4; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.00032;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIXY 28
DB 4 YELPELDYDAYDALEPHIAAEIMELHHS 30

RESULT 8
AAG92973
ID AAG92973 standard; protein; 200 AA.
XX AC AAG92973;
XX 26-SEP-2001 (first entry)
XX C glutamicum protein fragment SEQ ID NO: 6727.
XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis.
XX Corynebacterium glutamicum.
XX EP1108790-A2.
XX 20-JUN-2001.
XX 18-DEC-2000; 2000EP-00127688.
XX 16-DEC-1999; 99JP-00377484.
XX 07-APR-2000; 2000JP-00159162.
XX 03-AUG-2000; 2000JP-00280988.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX WPI; 2001-376931/40.
XX N-PSDB; AAH68192.
XX Novel polynucleotides derived from *Coryneform* bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analyzing
XX expression profile or pattern of a gene and identifying homologous gene.
XX Claim 17; SEQ ID NO 6727; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein sequences from the *Coryneform* bacterium *Corynebacterium glutamicum*. These are useful for identifying the mutation point of a gene derived from a mutant of *coryneform* bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from *Coryneform* bacterium, and identifying a homologue of a gene derived from *Coryneform* bacterium. *Coryneform* bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office

XX Sequence 200 AA;

Query Match 53.1%; Score 77; DB 4; Length 200;
Best Local Similarity 48.1%; Pred. No. 0.00032;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIXY 28
DB 4 YELPELDYDAYDALEPHIAAEIMELHHS 30

RESULT 9
AAE24641
ID AAE24641 standard; protein; 95 AA.

The present sequence is that of the 198 amino acid long hMn-SOD mature polypeptide having a Lys residue at position 29. The protein is produced with an N-terminal Met residue which is then removed, e.g. by treatment with CNBr or CMCl, to release mature hMn-SOD. The mature recombinant protein is useful for treating, preventing or diagnosing inflammatory, degenerative, neoplastic and rheumatic disorders; in wound healing and autoimmune diseases. (Updated on 25-MAR-2003 to correct PF field.)

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Sequence 198 AA;

[illegible]

	Query Match	51.0%; Score 74; DB 3; Length 198;
	Best Local Similarity	42.9%; Pred. No. 0.00098;
	Matches	12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY	1 KYSLPDLDFEFSATEPYISGQINEIXYT 28	
DB	1 KHSLPDLFDYDGALEPHINAIQMQLHHS 28	
	RESULT 18	
ID	AAR20015	
XX	AAAR20015 standard; protein; 199 AA.	
AC	AAR20015;	
DT	01-APR-1992 (first entry)	
DE	Mn-SOD (Ile59Thr).	
KW	Manganese superoxide dismutase; vector; anti-inflammatory.	
OS	Homo sapiens.	
FH	Key Location/Qualifiers	
FT	Misc-difference 59	
FT	/label= ILE->THR	
PX	EP462836-A.	
XX	27-DEC-1991.	
PF	20-JUN-1991; 91EP-00305596.	
PR	20-JUN-1990; 90JP-00159925.	
PR	19-OCT-1990; 90JP-00279286.	
PA	(MITK) MITSUI TOATSU CHEM INC.	
PI	Takahashi S, Makino T, Asanagi M, Yoshino C;	
DR	WPI; 1992-001187/01.	
DR	N-PSDB; AAQ20194.	
PT	New recombinant vector plasmid - expresses human manganese, superoxide	
PT	dismutase, used as antiinflammatory agent.	
PS	Disclosure; Fig 8; 22pp; English.	
CC	A vector was constructed contg. tac/pl ligated promoter which has a human	
CC	Mn-SOD structural gene. The gene encodes modified human Mn-SOD in which	
CC	the 59th isoleucine is converted to threonine	
SQ	Sequence 199 AA;	
	Query Match	51.0%; Score 74; DB 2; Length 199;
	Best Local Similarity	42.9%; Pred. No. 0.00098;
	Matches	12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY	1 KYSLPDLDFEFSATEPYISGQINEIXYT 28	
DB	2 KHSLPDLFDYDGALEPHINAIQMQLHHS 29	
	RESULT 19	
ID	AAR60359	
XX	AAAR60359 standard; protein; 199 AA.	
AC	AAR60359;	
DT	25-MAR-2003 (revised)	
DT	27-FEB-1995 (first entry)	
DE	MnSOD N-terminal.	

XX	Manganese superoxide dismutase; MnSOD; oxygen; cosmetic; mutation; arthritis; variant; enzyme; isoelectric point; inflammation; cancer; premature retinopathy; hypertension; diabetes.	
OS	Homo sapiens.	
PN	WO9414950-A1.	
PD	07-JUL-1994.	
XX	28-DEC-1993; 93WO-JP001917.	
XX	28-DEC-1992; 92JP-00359959.	
XX	(SIIT-) SII TECHNOSEARCH INC.	
PA	Kondo M, Katsuta K;	
PI	WPI; 1994-234688/28.	
DR	Human variant manganese super-oxide dismutase with aminoacid mutation in non-essential regions - for treatment of arthritis, active oxygen related disorders and for cosmetics.	
XX	Disclosure; Page 6-7; 34pp; Japanese.	
PS	Human variant manganese superoxide dismutase (Mn-SOD) comprises an amino acid substitution in a region which does not affect enzyme activity, of a positively charged amino acid residue, which has the effect of raising the isoelectric point of the peptide. These Mn-SOD variants are useful as medical preps. for the treatment of human arthritis and diseases caused by active oxygen, and as cosmetic preps. They are also useful for treatment of inflammation, cancer, premature retinopathy, hypertension and diabetes. Examples of variant Mn-SODs are given in AAQ70431-32. (Updated on 25-MAR-2003 to correct PN field.)	
CC	Sequence 199 AA;	
	Query Match	51.0%; Score 74; DB 2; Length 199;
	Best Local Similarity	42.9%; Pred. No. 0.00098;
	Matches	12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY	1 KYSLPDLDFEFSATEPYISGQINEIXYT 28	
DB	2 KHSLPDLFDYDGALEPHINAIQMQLHHS 29	
	RESULT 20	
ID	AAAP71701	
XX	AAAP71701 standard; protein; 222 AA.	
AC	AAAP71701;	
XX	25-MAR-2003 (revised)	
DT	10-MAR-2003 (revised)	
DT	14-MAY-1991 (first entry)	
XX	Recombinant human manganese superoxide dismutase.	
DE	Human MSOD; hydrogen peroxide; ischaemia; lesions; inflammation; free radicals.	
KW	Homo sapiens.	
XX	Key Location/Qualifiers	
FT	Protein 25..222	
FT	/label= mature MSOD	
XX	BE905796-A.	
PN	16-MAR-1987.	
PD		
XX		

PF 20-NOV-1986; 86BE-00905796.
XX
XX
PR 22-NOV-1985; 85US-00801051.
PR 22-NOV-1985; 85US-00801090.
PR 12-SEP-1986; 86US-00907051.
XX
XX (BIOT-) BIO-TECHNOL GEN.
PA
XX
XX WPI; 1987-101441/15.
DR N-PSDB; AAN71370.
XX
XX New DNA coding for polypeptide of human manganese superoxidizedismutase -
PT useful e.g. for treating inflammation, and new expression vectors and
PT transformed cells.
XX
XX
XX Disclosure; Fig 1; 46pp; French.
PS
XX This sequence comprises both prepro- and mature-manganese super- oxide
XX dismutase (MSOD). It is encoded by the sense strand of a double-stranded
CC molecule contained in a recombinant vehicle. This recombinant MSOD
CC catalyses the reaction of hydrogen ions and the SOD radical anion to form
CC hydrogen peroxide and water. It is useful in veterinary and
CC pharmaceutical compsns. for eg reducing lesions of reperfusion following
CC ischaemia, to prolong survival time isolated organs and for treating
CC inflammation. See also AAN71371-72. (Updated on 10-MAR-2003 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 222 AA;
XX
Query Match 51.0%; Score 74; DB 1; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYFESATEPYISQINEIXYT 28
Db 25 KHSLPDLPYDGALEPHINAQIMQLHHS 52
RESULT 21
AAR44801
ID AAR44801 standard; protein; 222 AA.
AC AAR44801;
XX
XX 25-MAR-2003 (revised)
DT 21-JUN-1994 (first entry)
XX
XX MnSOD cDNA.
DE
XX MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion;
KW injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
KW ss.
XX Homo sapiens.
OS
XX US5270195-A.
PN
XX 14-DEC-1993.
PD
XX 10-JUL-1992; 92US-00912213.
XX
XX 22-NOV-1985; 85US-00801090.
PR 12-SEP-1986; 86US-00907051.
PR 29-OCT-1986; 86IE-00002851.
PR 27-MAR-1987; 87US-00032734.
PR 13-DEC-1989; 89US-00453057.
XX
XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
PA
XX
XX Beck Y, Hartman JR;
PI
XX WPI; 1993-404931/50.
DR N-PSDB; AAO53193.
DR

XX Expression plasmid in Escherichia coli host system - encodes human
PT manganese superoxidizedismutase analogue, useful for e.g. treating
PT inflammation.
XX
XX Claim 1; Fig 1a-1c; 27pp; English.
XX
XX The sequence is of a maganese superoxide dismutase which can be used to
CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide
CC and molecular oxygen. It can be used to reduce reperfusion injury
CC following ischaemia and prolong the survival of excised organs. It can
CC also me used as a long acting anti-inflammatory drug. (Updated on 25-MAR-
CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 222 AA;
XX
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYFESATEPYISQINEIXYT 28
Db 25 KHSLPDLPYDGALEPHINAQIMQLHHS 52
RESULT 22
AAR61337
ID AAR61337 standard; protein; 222 AA.
XX
XX AAR61337;
AC
XX 25-MAR-2003 (revised)
DT 31-MAY-1995 (first entry)
XX
XX Human manganese-contg. superoxide dismutase SOD-2.
DE
XX Human superoxide dismutase; hSOD2; mSOD; neurodegeneration;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW Hallervorden-Spatz disease; olivopontocerebellar atrophy;
KW familial amyotrophic lateral sclerosis; FALS; diagnosis; mutant SOD;
KW reverse transcription polymerase chain reaction; SSCP analysis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
PH Peptide 1..18
FT /label= signal peptide
FT 19..222
FT Protein /label= mature_mSOD
FT
XX WO9419493-A1.
XX
XX 01-SEP-1994.
PD
XX 28-FEB-1994; 94WO-US002089.
XX
XX 26-FEB-1993; 93US-00023980.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Brown R, Horvitz HR, Rosen DR;
PI
XX WPI; 1994-294353/36.
DR N-PSDB; AAO67474.
DR
XX Diagnosis, treatment and prevention of diseases of cell death - e.g.
PT amyotrophic lateral sclerosis, which are the result of e.g. decreased SOD
PT activity.
XX
XX Claim 22; Fig 3; 94pp; English.
PS
XX The presence of a mutation in a gene encoding a superoxide dismutase
CC

CC (SOD1, SOD2 or SOD3) indicates an increased likelihood of developing a
 CC cell death disease, specifically a neurodegenerative disease. The use of
 CC SOD polypeptides to treat amyotrophic lateral sclerosis and diseases
 CC involving a deleterious mutation in the glutathione peroxidase-encoding
 CC gene, the catalase-encoding gene and the nitric oxide-encoding gene is
 CC claimed. The specification includes the sequences of human SOD1, hSOD2
 CC and hSOD3 (AAR61336- AAR61338, respectively). (Updated on 25-MAR-2003 to
 CC correct PN field.)

XX SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLDFEFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLPDYDGALEPHINAQIMQLHHS 52

RESULT 24

AAR75193
 ID AAR75193 standard; protein; 222 AA.

XX AAR75193;

XX 25-MAR-2003 (revised)

DT 23-MAY-1996 (first entry)

XX Human manganese superoxide dismutase (lys29) preprotein.

KW hMn-SOD; manganese; superoxide dismutase; tetramer; inflammation;
 KW autoimmune disease; rheumatoid arthritis; neoplasm; emphysema;
 KW osteoarthritis; wound healing; leader peptide; precursor.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..24

FT Protein /label= leader

FT /label= mature_hMnSOD_(Lys29)

XX EP676472-A1.

XX 11-OCT-1995.

XX 10-MAR-1988; 95EP-00107460.

XX 14-MAR-1987; 87DE-03708306.

XX 26-MAY-1987; 87DE-03717695.

XX 10-JUL-1987; 87DE-03722884.

XX 24-DEC-1987; 87DE-03744038.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX Heckl K, Spevak W, Ostermann E, Zoepfel A, Krystek E;

PI Maurer-Fogy I, Wiche-Castanon M, Strätowa C, Hauptmann R;

XX WPI; 1995-346092/45.

XX N-PSDB; AAQ94284.

PT Genes encoding recombinant human manganese superoxide dismutase - for
 PT treatment, prevention and diagnosis of inflammatory diseases.

XX Claim 8; Page 3-4 and Page 19-20; 54pp; German.

XX The present sequence is that of the 198 amino acid long hMn-SOD mature
 CC polypeptide having a Lys residue at position 29, preceded by a 24 amino
 CC acid residue leader peptide. Mature, recombinant hMn-SOD is useful for
 CC treating, preventing or diagnosing inflammatory, degenerative, neoplastic
 CC and rheumatic disorders; in wound healing and in autoimmune diseases.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDLDFEFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLPDYDGALEPHINAQIMQLHHS 52

RESULT 24

AAR90713

ID AAR90713 standard; protein; 222 AA.

XX AAR90713;

XX 25-MAR-2003 (revised)

DT 06-APR-1996 (first entry)

XX Human manganese superoxide-dismutase.

KW Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
 KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;
 KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;
 KW synovial inflammation; arthritis; lung fibrosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..24

FT Region /note= "Pre-peptide"

FT 39..48

FT /note= "Region used to construct probe AAT15591"

FT Misc-difference 66

FT /note= "Gln in previously published sequence"

FT Misc-difference 112

FT /note= "Gln in previously published sequence"

FT Misc-difference 132

FT /note= "Gln in previously published sequence"

FT Misc-difference 147..148

FT /note= "Residues not present in previously published sequence"

FT 203..213

FT /note= "Region used to construct probe AAT15592"

XX EP691401-A1.

XX 10-JAN-1996.

XX 25-MAR-1988; 95EP-00106995.

XX 27-MAR-1987; 87US-00032734.

XX 26-FEB-1988; 88US-00161117.

XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX Hartman JR, Beck Y, Nimrod A;

XX WPI; 1996-059735/07.

XX N-PSDB; AAT15589.

PT New human manganese superoxide dismutase analogues - having a Lys and
 PT opt. His residue absent from the N-terminus, useful for treating e.g.
 PT synovial inflammation, arthritis or lung fibrosis.

XX Example 1; Fig 1; 45pp; English.

XX The sequence represents a human manganese superoxide-dismutase (MnSOD),
 CC and is encoded by a human T-lymphocyte cDNA isolated from a library in
 CC phage lambda-gt10 in Escherichia coli, by screening with a 5'-probe
 CC (AAT15591) and a 3'-probe (AAT15592), followed by subcloning in plasmid

ID	AAW82446 standard; protein; 222 AA.
XX AC	AAW82446;
DT DT	24-FEB-1999 (first entry)
DE DE	Human mSOD protein.
KW KW	SOD1; SOD2; SOD3; Cu/Zn; superoxide dismutase; mitochondrial; treatment; extracellular; neurodegenerative disease; amyotrophic lateral sclerosis; familial; ALS.
OS OS	Homo sapiens.
PV PN	US5849290-A.
PD PD	15-DEC-1998.
PF PF	07-JUN-1995; 95US-00486953.
PR PR	26-FEB-1993; 93US-00023980. 28-FEB-1994; 94US-00204052.
PA PA	(MASI) MASSACHUSETTS INST TECHNOLOGY. (GBHO) GEN HOSPITAL CORP.
PI PI	Rosen DR, Brown R, Horvitz HR;
DR DR	WPI; 1999-069657/06.
NX NX	N-PSTD; AAV73824.
PT PT	Treatment of neurodegenerative disease - by administering super-oxide dismutase.
PS PS	Disclosure; Fig 3; 53pp; English.
CC CC	This sequence is a novel human mitochondrial SOD (superoxide dismutase) protein encoded by the SOD2 gene. This protein can be used in a method for treating a neurodegenerative disease particularly familial amyotrophic lateral sclerosis (ALS)
QY QY	Sequence 222 AA;
Dy Dy	Query March 51.0%; Score 74; DB 2; Length 222; Best Local Similarity 42.9%; Pred.No. 0.0011; Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps
Cy Cy	1 KYSLPEDYEFSATPEYISGQINEIXYT 28 :: :: :: :: :: :: :: : 25 KHSLPLDPVDYGALRPFHNAIMQLHHS 52
RESULT 29	
AAP98177	
ID ID	AAW98177 standard; protein; 222 AA.
XX XX	AAW98177;
AC AC	
XX XX	05-JUL-1999 (first entry)
DE DE	Human manganese superoxide dismutase H30S mutant.
XX XX	Superoxide dismutase; MnSOD; SOD; human; protein engineering; enzyme engineering; antioxidant; antiinflammatory; cytotoxicity; inflammation; reperfusion injury; therapy; mutant.
KW KW	Homo sapiens.
XN XN	Synthetic.
OS OS	
XX XX	Key Location/Qualifiers
FH FH	Peptide 1..24
FT FT	/note= "signal peptide"
FT FT	Protein 25..222

FT Active-site 98 /note= "Tyr-74"
FT Misc-difference 155 /label= Gln, Glu
FT Misc-difference 167 /note= "Gln replaces Asn in wild-type hMnSOD"
FT Active-site 167 /note= "Gln-143"
FT Active-site 183 /note= "Asp-159"
FT Active-site 185 /note= "Trp-161"
FT Active-site 187 /note= "His-163"
FT XX
PN W09913088-A1.
XX
XX 18-MAR-1999.
XX
XX 10-SEP-1998; 98WO-US018842.
XX
XX 10-SEP-1997; 97US-00927230.
XX
XX (UYFL) UNIV FLORIDA.
XX
XX Nick HS, Silverman DN;
XX
XX WPI; 1999-229242/19.
XX
XX New recombinant human manganese superoxide dismutase proteins.
XX
XX Claim 15; Page 54-55; 6lpp; English.
XX
XX This protein is a Q143N mutant of human manganese superoxide dismutase (hMnSOD, see also AAW98170). Novel modified hMnSOD proteins having catalytic activity which differs from natural hMnSOD are claimed. The modified proteins (see also AAW98172-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30 are located near the active site metal, are highly conserved, and are involved in a hydrogen bond relay which links the active site metal-bound hydroxyl group to ordered solvent, and are thus all potentially involved in catalytic activity, product inhibition and/or enzyme stability. The particularly preferred Q143N mutant has a kcat of 0.3 m/sec and a kcat/km of 0.82/uM.sec compared to respective values of 40 m/sec and 800/uM.sec for wild-type hMnSOD. It exhibits no product inhibition. Modified hMnSODs, or expression vectors in which a modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents

Qy 1 KYSPELDYFSATPEYTSQGINEIXYT 28
Db 25 KHSLPDLPYDYGALEPHINAQIMQLHS 52

RESULT 33
AAW98170
ID AAW98170 standard; protein; 222 AA.
XX
AC AAW98170;

XX 05-JUL-1999 (first entry)
XX Human native manganese superoxide dismutase.
XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
XX enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
XX inflammation; reperfusion injury; therapy.
XX Homo sapiens.
XX Key
XX Peptide 1..24
XX /note= "signal peptide"
XX Protein 25..222
XX /note= "mature protein"
XX 50
XX Active-site /note= "His-26"
XX 54
XX Active-site /note= "His-30"
XX 58
XX Active-site /note= "Tyr-58"
XX 98
XX Active-site /note= "Tyr-74"
XX Misc-difference 155 /label= Gln, Glu
XX 167
XX Active-site /note= "Gln-143"
XX 183
XX Active-site /note= "Asp-159"
XX 185
XX Active-site /note= "Trp-161"
XX 187
XX Active-site /note= "His-163"
XX
XX W09913088-A1.
XX
XX 18-MAR-1999.
XX
XX 10-SEP-1998; 98WO-US018842.
XX
XX 10-SEP-1997; 97US-00927230.
XX
XX (UYFL) UNIV FLORIDA.
XX
XX Nick HS, Silverman DN;
XX
XX WPI; 1999-229242/19.
XX
XX New recombinant human manganese superoxide dismutase proteins.
XX
XX Claim 2; Page 53-54; 6lpp; English.
XX
XX This protein is human manganese superoxide dismutase (hMnSOD). Novel hMnSOD proteins having catalytic activity which differs from this natural hMnSOD are claimed (see AAW98171-77). The modified proteins exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. The modified hMnSOD, or expression vectors in which modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can be used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSPELDYFSATPEYTSQGINEIXYT 28
Db 25 KHSLPDLPYDYGALEPHINAQIMQLHS 52

RESULT 33
AAW98170
ID AAW98170 standard; protein; 222 AA.
XX
AC AAW98170;

Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISQINEIXYT 28
 Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 34

AAW98174
 ID AAW98174 standard; protein; 222 AA.

XX AC AAW98174;

XX 05-JUL-1999 (first entry)

XX Human manganese superoxide dismutase Q143D mutant.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy; mutant.

XX Homo sapiens.

XX Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..24

FT /note= "signal peptide"

FT Protein 25..222

FT /note= "mature protein"

FT Active-site 50

FT /note= "His-26"

FT Active-site 54

FT /note= "His-30"

FT Active-site 58

FT /note= "Tyr-58"

FT Active-site 98

FT /note= "Tyr-74"

FT Misc-difference 155

FT /label= Gln, Glu

FT Misc-difference 167

FT /note= "Gln replaces Asp in wild-type hMnSOD"

FT Active-site 167

FT /note= "Gln-143"

FT Active-site 183

FT /note= "Asp-159"

FT Active-site 185

FT /note= "Trp-161"

FT Active-site 187

FT /note= "His-163"

XX WO9913088-A1.

PN 18-MAR-1999.

XX 10-SEP-1998; 98WO-US018842.

PF 10-SEP-1997; 97US-00927230.

PR (UYFL) UNIV FLORIDA.

PA Nick HS, Silverman DN;

PI WPI; 1999-229242/19.

XX New recombinant human manganese superoxide dismutase proteins.

XX Claim 14; Page; 61pp; English.

XX This protein is a Q143D mutant of human manganese superoxide dismutase

CC (hMnSOD; see also AAW98170). Novel modified hMnSOD proteins having

CC catalytic activity which differs from natural hMnSOD are claimed. The

CC modified proteins (see also AAW98171-77) exhibit reduced or no product

CC inhibition, or have greater activity, or both, compared to natural

CC hMnSOD. The modifications involve one or amino acid substitutions within
 CC the active site of the enzyme, especially at residues His-26, His-30, Tyr
 CC -34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and
 CC His-30 are located near the active site metal, are highly conserved, and
 CC are involved in a hydrogen bond relay which links the active site metal-
 CC bound hydroxyl group to ordered solvent, and are thus all potentially
 CC involved in catalytic activity, product inhibition and/or enzyme
 CC stability. Modified hMnSODs, or expression vectors in which a modified
 CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are
 CC used to protect a cell line from damage caused by superoxide radicals
 CC (claimed). They can also be used to treat subjects suffering from, or at
 CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury following
 CC ischemia (claimed), and cellular damage caused by chemotherapeutic
 CC agents. Note. The present sequence is not shown in the specification but
 CC is derived from the hMnSOD sequence given on page 53-54
 XX SQ Sequence 222 AA;

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.0011;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISQINEIXYT 28

Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 35

AAW98169

ID AAW98169 standard; protein; 222 AA.

XX AC AAW98169;

XX 05-JUL-1999 (first entry)

DE Human native manganese superoxide dismutase.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24

FT /note= "signal peptide"

FT Protein 25..222

FT /note= "mature protein"

FT Active-site 50

FT /note= "His-26"

FT Active-site 54

FT /note= "His-30"

FT Active-site 58

FT /note= "Tyr-58"

FT Active-site 98

FT /note= "Tyr-74"

FT Active-site 167

FT /note= "Gln-143"

FT Active-site 183

FT /note= "Asp-159"

FT Active-site 185

FT /note= "Trp-161"

FT Active-site 187

FT /note= "His-163"

XX WO9913088-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US018842.

PR 10-SEP-1997; 97US-00927230.
XX (UYFL) UNIV FLORIDA.
XX Nick HS, Silverman DN;
XX WPI; 1999-229242/19.
XX N-PSDB; AAX24998.
XX New recombinant human manganese superoxide dismutase proteins.
PT
XX
XX Disclosure; Page 52-53; 61pp; English.
XX
XX This protein is human manganese superoxide dismutase (hMnSOD). Novel
CC hMnSOD proteins having catalytic activity which differs from this natural
CC hMnSOD are claimed (see AAW98171-77). The modified proteins exhibit
CC reduced or no product inhibition, or have greater activity, or both,
CC compared to natural hMnSOD. The modifications involve one or amino acid
CC substitutions within the active site of the enzyme, especially at
CC residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
CC His-163. The modified hMnSOD, or expression vectors in which modified
CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can
CC be used to protect a cell line from damage caused by superoxide radicals
CC (claimed). They can also be used to treat subjects suffering from, or at
CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
CC they can be used as antioxidants in the treatment of a variety of
CC disorders, including inflammation (claimed), reperfusion injury following
CC ischemia (claimed), and cellular damage caused by chemotherapeutic agents
XX
XX Sequence 222 AA;
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYFSATEPYISQINEIXYT 28
DB 25 KHSLEPDLFYDYGALPEHINAQIMQLHHS 52
RESULT 36
AAW98173
ID AAW98173 standard; protein; 222 AA.
AC AAW98173;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human manganese superoxide dismutase Q143H mutant.
XX
XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1. .24
FT Peptide /note= "signal peptide"
FT Protein 25. .222
FT /note= "mature protein"
FT Active-site 50
FT /note= "His-26"
FT Active-site 54
FT /note= "His-30"
FT Active-site 58
FT /note= "Tyr-58"
FT Active-site 98
FT /note= "Tyr-74"
FT Misc-difference 155
FT /label= Gln, Glu
FT Misc-difference 167

FT Active-site 167
FT /note= "Gln-143"
FT Active-site 183
FT /note= "Asp-159"
FT Active-site 185
FT /note= "Trp-161"
FT Active-site 187
FT /note= "His-163"
XX
XX WO9913088-A1.
XX
XX 18-MAR-1999.
XX
XX 10-SEP-1998; 98WO-USO18842.
XX
XX 10-SEP-1997; 97US-00927230.
XX (UYFL) UNIV FLORIDA.
XX Nick HS, Silverman DN;
XX WPI; 1999-229242/19.
XX New recombinant human manganese superoxide dismutase proteins.
XX Claim 14; Page; 61pp; English.
XX
XX This protein is a Q143H mutant of human manganese superoxide dismutase
CC (hMnSOD, see also AAW98170). Novel modified hMnSOD proteins having
CC catalytic activity which differs from natural hMnSOD are claimed. The
CC modified proteins (see also AAW98171-77) exhibit reduced or no product
CC inhibition, or have greater activity, or both, compared to natural
CC hMnSOD. The modifications involve one or amino acid substitutions within
CC the active site of the enzyme, especially at residues His-26, His-30, Tyr
CC -34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and
CC His-30 are located near the active site metal, are highly conserved, and
CC are involved in a hydrogen bond relay which links the active site metal-
CC bound hydroxyl group to ordered solvent, and are thus all potentially
CC involved in catalytic activity, product inhibition and/or enzyme
CC stability. Modified hMnSODs, or expression vectors in which a modified
CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are
CC used to protect a cell line from damage caused by superoxide radicals
CC (claimed). They can also be used to treat subjects suffering from, or at
CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
CC they can be used as antioxidants in the treatment of a variety of
CC disorders, including inflammation (claimed), reperfusion injury following
CC ischemia (claimed), and cellular damage caused by chemotherapeutic
CC agents. Note. The present sequence is not shown in the specification but
CC is derived from the hMnSOD sequence given on page 53-54
XX
XX Sequence 222 AA;
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0011;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 KYSLPELDYFSATEPYISQINEIXYT 28
DB 25 KHSLEPDLFYDYGALPEHINAQIMQLHHS 52
RESULT 37
AAW98176
ID AAW98176 standard; protein; 222 AA.
XX
XX AAW98176;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human manganese superoxide dismutase H30N mutant.
XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW

QY
1 KYSLPDYEFSA TE PYISGQINEIXYT 28

db 25 KHSLPDLPDYGALEPHINAQIMQLHHS 52

Thu Sep 2 12:32:51 2004

us-09-987-190-2.rag

Page 21

Search completed: August 24, 2004, 23:00:36
Job time : 126 secs

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OM protein - protein search, using sw model

Run on: August 24, 2004, 22:58:32 ; Search time 31 Seconds
(without alignments)
49.961 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYEFSAPEYISGQINEIXYXX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*
 - 2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*
 - 3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*
 - 4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	4	US-09-262-856A-2
2	103	71.0	207	4	US-09-214-909-24
3	100	69.0	233	2	US-08-928-692-31
4	100	69.0	233	4	US-09-339-972-31
5	79	54.5	30	4	US-09-091-097-52
6	79	54.5	224	4	US-09-091-097-8
7	77	53.1	200	4	US-09-373-731-2
8	74	51.0	198	3	US-09-075-019-2
9	74	51.0	198	6	5240847-10
10	74	51.0	198	6	5240847-11
11	74	51.0	222	2	US-08-365-486A-28
12	74	51.0	222	2	US-08-023-980B-44
13	74	51.0	222	2	US-08-486-953A-52
14	74	51.0	222	2	US-08-927-230A-2
15	74	51.0	222	2	US-08-927-230A-3
16	74	51.0	222	3	US-09-151-052-2
17	74	51.0	222	3	US-09-151-052-3
18	74	51.0	222	3	US-09-126-109-2
19	74	51.0	222	3	US-08-880-342-28
20	74	51.0	226	3	US-09-075-019-7
21	71	49.0	188	4	US-09-262-856A-6
22	70	48.3	46	6	5240847-24
23	70	48.3	214	4	US-09-198-452A-75
24	69	47.6	230	2	US-08-928-692-30
25	69	47.6	230	4	US-09-339-972-30
26	66	45.5	22	4	US-09-157-689-23
27	63	43.4	217	4	US-09-489-039A-12227

28	62	42.8	206	4	US-09-091-097-6	Sequence 6, Appli
29	58	40.0	214	3	US-09-411-578-1	Sequence 1, Appli
30	58	40.0	214	4	US-09-749-233-1	Sequence 1, Appli
31	58	40.0	224	4	US-09-543-681A-6654	Sequence 6654, Ap
32	58	40.0	241	4	US-09-540-236-3442	Sequence 3442, Ap
33	57	39.3	201	4	US-09-134-001C-3584	Sequence 3584, Ap
34	56	38.6	190	4	US-08-679-493A-184	Sequence 184, App
35	55	37.9	205	4	US-09-543-681A-4456	Sequence 4456, Ap
36	54	37.2	245	4	US-09-252-991A-24333	Sequence 24333, A
37	53	36.6	204	1	US-08-445-909A-17	Sequence 17, Appl
38	53	36.6	204	1	US-08-445-909A-29	Sequence 29, Appl
39	52	35.9	207	4	US-09-252-991A-24593	Sequence 24593, A
40	50	34.5	371	4	US-09-636-215-708	Sequence 708, App
41	50	34.5	371	4	US-09-685-166A-708	Sequence 708, App
42	50	34.5	400	4	US-09-636-215-852	Sequence 852, App
43	50	34.5	400	4	US-09-685-166A-852	Sequence 852, App
44	50	34.5	553	3	US-09-020-956-113	Sequence 113, App
45	50	34.5	553	3	US-09-030-607-113	Sequence 113, App

ALIGNMENTS

RESULT 1

US-09-262-856A-2
; Sequence 2, Application US/09262856A
; Patent No. 633164
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutoh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikuroshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-372P
; CURRENT APPLICATION NUMBER: US/09/262,856A
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; OTHER INFORMATION: residues 26, 39, 30 = unknown
US-09-262-856A-2

Query Match 97.2%; Score 141; DB 4; Length 30;
Best Local Similarity 100.0%; Pred No. 1.6e-16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXYT 28
DB 1 KYSLPELDYEFSAPEYISGQINEIXYT 28

RESULT 2

US-09-214-909-24
; Sequence 24, Application US/09214909
; Patent No. 6486382
; GENERAL INFORMATION:
; APPLICANT: GORDON-KAMM, WILLIAM
; APPLICANT: PIERCE, DOROTHY A.
; APPLICANT: BOWEN, BENJAMIN
; APPLICANT: BIDNEY, DENNIS
; APPLICANT: ROSS, MARGIT
; APPLICANT: SCELONGE, CHRISTOPHER
; APPLICANT: MILLER, MICHAEL D.
; APPLICANT: SANDAHL, GARY
; APPLICANT: WANG, LIJUAN
; TITLE OF INVENTION: USE OF THE GREEN FLUORESCENT PROTEIN AS A SCREENABLE
; FILE REFERENCE: 03329/0682
; CURRENT APPLICATION NUMBER: US/09/214,909

```

; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/07688
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 60/016,345
; PRIOR FILING DATE: 1996-05-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Superoxide
; OTHER INFORMATION: dismutase fused to GFPm
US-09-214-909-24

Query Match 71.0%; Score 103; DB 4; Length 207;
Best Local Similarity 60.7%; Pred. No. 3.7e-09;
Matches 17; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYSLPDYFSGATEPYISQINEIXYT 28
Db 3 EYTLPLDYDYSALEPHISQINELHHS 30

RESULT 3
US-08-928-692-31
; Sequence 31, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5958727e
US-08-928-692-31

Query Match 69.0%; Score 100; DB 2; Length 233;
Best Local Similarity 64.3%; Pred. No. 1.3e-08;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPDYFSGATEPYISQINEIXYT 28
Db 3 EYTLPLDYDYSALEPHISQINELHHS 30

RESULT 4
US-09-339-972-31
; Sequence 31, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6323002e
US-09-339-972-31

Query Match 69.0%; Score 100; DB 4; Length 233;
Best Local Similarity 64.3%; Pred. No. 1.3e-08;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPDYFSGATEPYISQINEIXYT 28
Db 27 KVTLPDLKWDGFALEPYISQINELHHT 54

RESULT 5
US-09-091-097-52
; Sequence 52, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
US-09-091-097-52
```

APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-091-097-52

Query Match 54.5%; Score 79; DB 4; Length 30;
Best Local Similarity 55.6%; Pred. No. 2.8e-06;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXY 27
DB 1 KYTLPLPDYDYGALPAISGEINETHY 27

RESULT 6

US-09-091-097-8
Sequence 8, Application US/09091097
Patent No. 6432407
GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZUTOH
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-097-8

Query Match 54.5%; Score 79; DB 4; Length 224;
Best Local Similarity 55.6%; Pred. No. 3.8e-05;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSSATEPYISQINEIXY 27
DB 25 KYTLPLPDYDYGALPAISGEINETHY 51

RESULT 7

US-09-373-731-2
Sequence 2, Application US/09373731
Patent No. 6569650
GENERAL INFORMATION:
APPLICANT: DEGUSSA-HULS AG
APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
TITLE OF INVENTION: A PROCESS FOR THE FERMENTATIVE PREPARATION OF METABOLIC
TITLE OF INVENTION: PRODUCTS AND FOR THE NUCLEOTIDE SEQUENCES ENCODING FOR
TITLE OF INVENTION: THE SOD GENE
FILE REFERENCE: MERKAMM
CURRENT APPLICATION NUMBER: US/09/373,731
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 200
TYPE: PRT
ORGANISM: Corynebacterium melassecola
US-09-373-731-2

Query Match 53.1%; Score 77; DB 4; Length 200;
Best Local Similarity 48.1%; Pred. No. 7e-05;
Matches 13; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIXY 28
DB 4 YELPELDYDALEPHIAAEIMELHHS 30

RESULT 8

US-09-075-019-2
Sequence 2, Application US/09075019
Patent No. 6190658
GENERAL INFORMATION:
APPLICANT: UTC IR459
TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO

```

; LENGTH: 198
;
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-075-019-2
;
Query Match 51.0%; Score 74; DB 3; Length 198;
Best Local Similarity 42.9%; Pred. No. 0.00022;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
;
QY 1 KYSLPDLYEFSATEPYISGQINEIXYT 28
|:||||| |:| |:| |:| |:| |:| |:| :
Db 1 KHSPLDPDYDGALPHINAQMQLHHS 28
|:||||| |:| |:| |:| |:| |:| |:| :
;
RESULT 11
US-08-365-486A-28
; Sequence 28, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-28
;
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
;
QY 1 KYSLPDLYEFSATEPYISGQINEIXYT 28
|:||||| |:| |:| |:| |:| |:| |:| :
Db 25 KHSPLDPDYDGALPHINAQMQLHHS 52
|:||||| |:| |:| |:| |:| |:| |:| :
;
RESULT 12
US-08-023-980B-44
; Sequence 44, Application US/08023980B
; Patent No. 5843641
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 45
;

```



```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 585 Commercial Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-1024
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,980B
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/177001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-023-980B-44
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 13
US-08-486-953A-52
; Sequence 52, Application US/08486953A
; Patent No. 5849290
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,052
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/177001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-023-980B-44
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
; US-08-927-230A-2
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
; US-08-927-230A-2
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
; US-08-927-230A-2
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
; US-08-927-230A-2
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: OTHER
; LOCATION: 131
; OTHER INFORMATION: Xaa can code for Gln or Glu
; US-08-927-230A-2
Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.00025;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSATEPYISGQINEIXYT 28
Db 25 KHSLPDLPDYGALEPHINAQMQLHHS 52

RESULT 14
US-08-927-230A-2
; Sequence 2, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRES
```

QY 1 KYSLPDYFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 15

US-08-927-230A-3
 ; Sequence 3, Application US/08927230A
 ; Patent No. 5985633
 ; GENERAL INFORMATION:
 ; APPLICANT: Nick et al.
 ; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street, Floor 24
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/927,230A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: UFJ-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: OTHER
 ; LOCATION: 131
 ; OTHER INFORMATION: Xaa can code for Gln or Glu

US-08-927-230A-3

Query Match 51.0%; Score 74; DB 2; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00025;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 16

US-09-151-052-2
 ; Sequence 2, Application US/09151052
 ; Patent No. 6107070
 ; GENERAL INFORMATION:
 ; APPLICANT: Nick et al.
 ; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street, Floor 24
 ; CITY: Boston
 ; STATE: Massachusetts

; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/151,052
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/927,230
 ; FILING DATE: September 10, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: UFJ-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: OTHER
 ; LOCATION: 131
 ; OTHER INFORMATION: Xaa can code for Gln or Glu

US-09-151-052-2
 Query Match 51.0%; Score 74; DB 3; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.00025;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYFSATEPYISQINEIXYT 28
 Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 17

US-09-151-052-3
 ; Sequence 3, Application US/09151052
 ; Patent No. 6107070
 ; GENERAL INFORMATION:
 ; APPLICANT: Nick et al.
 ; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street, Floor 24
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/151,052
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/927,230
 ; FILING DATE: September 10, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: UFJ-001


```

Query Match      48.3%; Score 70; DB 4; Length 214;
Best Local Similarity 61.9%; Pred. No. 0.0011;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 YSLPELDYEFSEATEPYISGOI 22
      ||||| ||: || ||: ||: ||
Db      13 YSLPELDYDYDALEPVISSEI 33

RESULT 24
US-08-928-692-30
; Sequence 30, Application US/08928692
; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Brody, Deborah S.
; APPLICANT: Yaver, Deborah A.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
;

```

[illegible]

TITLE OF INVENTION: Abundant Extracellular Products and
 TITLE OF INVENTION: Methods for Their Production and Use
 NUMBER OF SEQUENCES: 95
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kurt A. MacLean
 STREET: 2029 Century Park East, Suite 3800
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.

```

1 ZIP: 90067
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: Patent In Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/09/157,689
16
17 FILING DATE:
18
19 CLASSIFICATION:
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: US 08/568,357
24
25 FILING DATE: 06-DEC-1995
26
27 PRIOR APPLICATION DATA:
28
29 APPLICATION NUMBER: US 08/551,149
30
31 FILING DATE: 31-OCT-1995
32
33 PRIOR APPLICATION DATA:
34
35 APPLICATION NUMBER: US 08/447,398
36
37 FILING DATE: 23-MAY-1995
38
39 PRIOR APPLICATION DATA:
40
41 APPLICATION NUMBER: US 08/289,667
42
43 FILING DATE: 12-AUG-1994
44
45 PRIOR APPLICATION DATA:
46
47 APPLICATION NUMBER: US 08/156,358
48
49 FILING DATE: 23-NOV-1993
50
51 ATTORNEY/AGENT INFORMATION:
52
53 NAME: MacLean, Kurt A.
54
55 REGISTRATION NUMBER: 31,118
56
57 REFERENCE/DOCKET NUMBER: 118-119
58
59 TELECOMMUNICATION INFORMATION:
60
61 TELEPHONE: (310) 788-5000
62
63 TELEFAX: (310) 277-1297
64
65 INFORMATION FOR SEQ ID NO: 23:
66
67 SEQUENCE CHARACTERISTICS:

```

```

;
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
;
US-09-157-689-23

Query Match 45.5%; Score 66; DB 4; Length 22;
Best Local Similarity 61.1%; Pred. No. 0.00026;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 LPDLDFEFSATEPYISQ 21
Db 5 LPDLWDYGALEPHISQ 22

RESULT 27
US-09-489-039A-12227
; Sequence 12227, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12227
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12227

Query Match 43.4%; Score 63; DB 4; Length 217;
Best Local Similarity 44.4%; Pred. No. 0.016;
Matches 12; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEPYISGQINEIXYT 28
Db 14 YTLFSLPYAYDALEPHFDKQTMETHT 40

RESULT 28
US-09-091-097-6
; Sequence 6, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA

;
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-091-097-6

Query Match 42.8%; Score 62; DB 4; Length 206;
Best Local Similarity 40.7%; Pred. No. 0.022;
Matches 11; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEPYISGQINEIXY 27
Db 6 EYTLPLPYAYDALEPFISKEIMTVHH 32

RESULT 29
US-09-411-578-1
; Sequence 1, Application US/09411578
; Patent No. 6203801
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/411,578
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 98203384.7
; EARLIER FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: 98203457.1
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Eimeria tenella
US-09-411-578-1

Query Match 40.0%; Score 58; DB 3; Length 214;
Best Local Similarity 46.2%; Pred. No. 0.11;
Matches 12; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEPYISGQINEIXY 27
Db 3 FELPPLPYEMDALEPFYSKETLEYHY 28

RESULT 30
US-09-749-233-1
; Sequence 1, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:
```

; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/411,578
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Eimeria tenella
US-09-749-233-1

Query Match 40.0%; Score 58; DB 4; Length 214;
Best Local Similarity 46.2%; Pred. No. 0.11;
Matches 12; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 27
Db 3 FELPPLPYMDALEPYISKETLEYHY 28

RESULT 31
US-09-543-681A-6654
; Sequence 6654, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6654
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6654

Query Match 40.0%; Score 58; DB 4; Length 224;
Best Local Similarity 40.7%; Pred. No. 0.11;
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 28
Db 20 YTLPALPYAYDALEPHDFDERTWEIHT 46

RESULT 32
US-09-540-236-3442
; Sequence 3442, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3442
; LENGTH: 241
; TYPE: PRT
; ORGANISM: M. catarrhalis

US-09-540-236-3442

Query Match 40.0%; Score 58; DB 4; Length 241;
Best Local Similarity 37.0%; Pred. No. 0.12;
Matches 10; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 28
Db 39 FTLPGLGYSDALEPHDFDKETMEIHS 65

RESULT 33

US-09-134-001C-3584
; Sequence 3584, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3584
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3584

Query Match 39.3%; Score 57; DB 4; Length 201;
Best Local Similarity 42.3%; Pred. No. 0.14;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 27
Db 5 FELPPLPYAYDALEPHDKQTWEIHH 30

RESULT 34

US-08-679-493A-184
; Sequence 184, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 184
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Entamoeba dispar
US-08-679-493A-184

Query Match 38.6%; Score 56; DB 4; Length 190;
Best Local Similarity 38.5%; Pred. No. 0.19;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 27
Db 3 FOLPQLPYAYNALEPHISKETLEPHH 28

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RESULT 35
US-09-543-681A-4456
; Sequence 4456, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4456
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4456
Query Match 37.9%; Score 55; DB 4; Length 205;
Best Local Similarity 42.3%; Pred. No. 0.31;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISGQINEIXY 27
Db 16 FELPKLPYDALEPHISKETLEYHY 41

RESULT 36
US-09-252-991A-24333
; Sequence 24333, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24333
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24333
Query Match 37.2%; Score 54; DB 4; Length 245;
Best Local Similarity 47.8%; Pred. No. 0.57;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISGQINE 24
Db 55 FELPLPYEKNALEPHISAETLE 77

RESULT 37
US-08-445-909A-17
; Sequence 17, Application US/08445909A
; Patent No. 5772996
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, Antony
; TITLE OF INVENTION: Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Superoxide Dismutase from Bacillus
; TITLE OF INVENTION: Stearotherophilus and Bacillus Caldotenax
; NUMBER OF SEQUENCES: 29
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
US-08-445-909A-17
Query Match 36.6%; Score 53; DB 1; Length 204;
Best Local Similarity 37.0%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISGQINEIXYT 28
Db 3 FELPALPYDYDALEPHIDKETMNIHT 29

RESULT 38
US-08-445-909A-29
; Sequence 29, Application US/08445909A
; Patent No. 5772996
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, Antony
; TITLE OF INVENTION: Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Superoxide Dismutase from Bacillus
; TITLE OF INVENTION: Stearotherophilus and Bacillus Caldotenax
; NUMBER OF SEQUENCES: 29
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,909A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,697
; FILING DATE: 02-FEB-1993
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-445-909A-29
Query Match 36.6%; Score 53; DB 1; Length 204;
Best Local Similarity 37.0%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISGQINEIXYT 28
Db 3 FELPALPYDYDALEPHIDKETMNIHT 29

RESULT 39
US-09-252-991A-24593
; Sequence 24593, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
```


/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.1136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 24593
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24593

Query Match 35.9%; Score 52; DB 4; Length 207;
Best Local Similarity 37.0%; Pred.No. 0.99;
Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEXYT 28
Db 7 HAUPPLPYDALEPHIDALTMEIHHS 33

RESULT 40
US-09-636-215-708
/ Sequence 708, Application US/09636215
/ Patent No. 6620922
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiangchun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.42717C17
/ CURRENT APPLICATION NUMBER: US/09/636,215
/ CURRENT FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 852
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 708
/ LENGTH: 371
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-636-215-708

Query Match 34.5%; Score 50; DB 4; Length 371;
Best Local Similarity 45.0%; Pred.No. 4.5;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQ 21
Db 150 YLLPAIDWDTALAPYLGTQ 169

Search completed: August 24, 2004, 23:04:24
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:01:08 ; Search time 124 Seconds
(without alignments)
76.029 Million cell updates/sec

Title: US-09-987-190-2

Perfect score: 145

Sequence: 1 KYSLPELDYFSAPEYISQINEIXYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	97.2	30	9	US-09-987-190-2
2	100	69.0	233	14	US-10-230-331-28
3	79	54.5	30	14	US-10-109-670-52
4	79	54.5	224	14	US-10-109-670-11
5	79	54.5	240	12	US-10-424-599-233245
6	77	53.1	200	9	US-09-818-564-2
7	77	53.1	200	9	US-09-738-626-6727
8	77	53.1	202	14	US-10-230-331-21
9	77	53.1	241	12	US-10-424-599-233247
10	74	51.0	95	9	US-09-993-333-12
11	74	51.0	183	16	US-10-752-791-2
12	74	51.0	222	14	US-10-230-331-19
13	74	51.0	222	14	US-10-230-331-20
14	74	51.0	222	14	US-10-230-331-22
15	74	51.0	222	16	US-10-408-765A-2109

16	72	49.7	228	14	US-10-230-331-25	Sequence 25, Appl
17	71	49.0	188	9	US-09-987-190-6	Sequence 6, Appl
18	70	48.3	214	15	US-10-289-762-75	Sequence 75, Appl
19	70	48.3	233	14	US-10-230-331-24	Sequence 24, Appl
20	68	46.9	213	14	US-10-156-761-12947	Sequence 12947, A
21	67	46.2	198	9	US-09-727-855B-7	Sequence 7, Appl
22	67	46.2	233	15	US-10-310-154-662	Sequence 662, App
23	67	46.2	235	14	US-10-230-331-26	Sequence 26, Appl
24	66	45.5	22	9	US-09-953-510-23	Sequence 23, Appl
25	66	45.5	22	11	US-09-953-413-23	Sequence 23, Appl
26	66	45.5	22	14	US-10-147-255-23	Sequence 23, Appl
27	66	45.5	222	9	US-09-727-855B-5	Sequence 5, Appl
28	65	44.8	80	12	US-10-424-599-184874	Sequence 184874, Appl
29	65	44.8	200	14	US-10-230-331-27	Sequence 27, Appl
30	62	42.8	206	14	US-10-109-670-10	Sequence 10, Appl
31	58	40.0	191	14	US-10-230-331-16	Sequence 16, Appl
32	58	40.0	191	14	US-10-230-331-29	Sequence 29, Appl
33	53	36.6	685	14	US-10-130-973A-7	Sequence 7, Appl
34	53	36.6	882	14	US-10-130-973A-4	Sequence 4, Appl
35	53	36.6	882	14	US-10-130-973A-3	Sequence 3, Appl
36	52.5	36.2	256	12	US-10-425-114-51507	Sequence 51507, A
37	52	35.9	201	15	US-10-310-154-664	Sequence 664, App
38	52	35.9	633	15	US-10-369-493-6225	Sequence 6225, App
39	51.5	35.5	384	16	US-10-437-963-163657	Sequence 163657, Sequence 163658,
40	51.5	35.5	770	16	US-10-437-963-163658	Sequence 188362,
41	51	35.2	171	12	US-10-424-599-188362	Sequence 5329, App
42	51	35.2	616	15	US-10-369-493-5329	Sequence 5, Appl
43	50	34.5	326	14	US-10-005-907-5	Sequence 974, App
44	50	34.5	359	9	US-09-822-827-974	Sequence 974, App
45	50	34.5	359	9	US-09-895-793-974	Sequence 974, App

ALIGNMENTS

RESULT 1
US-09-987-190-2
; Sequence 2, Application US/09987190
; Patent No. US20020058293A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, Kazutosh
; APPLICANT: MIZUTANI, Shigetoshi
; APPLICANT: ENDO, Masahiro
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: FUNGAL ANTIGENS AND PROCESS FOR PRODUCING THE SAME
; FILE REFERENCE: 1422-0502P
; CURRENT APPLICATION NUMBER: US/09/987,190
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/262,856
; PRIOR FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (1)..(30)
; OTHER INFORMATION: any Xaa = any amino acid, unknown or other
US-09-987-190-2

Query Match 97.2%; Score 141; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAPEYISQINEIXY 28

DB 1 KYSLPELDYFSAPEYISQINEIXY 28

RESULT 2

US-10-230-331-28

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; Sequence 28, Application US/10230331
; Publication No. US200301057513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-230-331-28

Query Match          69.0%; Score 100; DB 14; Length 233;
Best Local Similarity 64.3%; Pred. No. 8.1e-07;
Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KYSLPELDYFESATEPYISGQINEIXYT 28
   |||||::||| ||||| ||||| ||
Db 27 KYTLPLDKWDFGALEPYISGQINELHYT 54

RESULT 3
US-10-109-670-52
; Sequence 52, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 52
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-52

Query Match          54.5%; Score 79; DB 14; Length 30;
Best Local Similarity 55.6%; Pred. No. 0.00012;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYFESATEPYISGQINEIXY 27
   |||||::||| ||||| ||||| ||
Db 1 KYTLPLPYDYGALPAISGIMETHY 27

RESULT 4
US-10-109-670-11
; Sequence 11, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-11

Query Match          54.5%; Score 79; DB 14; Length 224;
Best Local Similarity 55.6%; Pred. No. 0.0011;
Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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US-10-424-599-233247
; Sequence 233247, Application US/10424599

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RESULT 11
US-10-752-791-2
; Sequence 2, Application US/10752791
; Publication No. US20040152115A1
; GENERAL INFORMATION:
; APPLICANT: Anziano, Paul Q.
; TITLE OF INVENTION: Manganese Superoxide
; TITLE OF INVENTION: and Nucleic Acid
; FILE REFERENCE: 53073-0001-US
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/621

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; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/075,948
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: PCT/US99/04129
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-752-791-2

Query Match      51.0%; Score 74; DB 16; Length 183;
Best Local Similarity 42.9%; Pred. No. 0.005;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 12
US-10-230-331-19
; Sequence 19, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-331-19

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 13
US-10-230-331-20
; Sequence 20, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-230-331-20

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 14
US-10-230-331-22
; Sequence 22, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-230-331-22

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 15
US-10-408-765A-2109
; Sequence 2109, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2109
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2109

Query Match      51.0%; Score 74; DB 16; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 16
US-10-230-331-25
; Sequence 25, Application US/10230331

```

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Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 14
US-10-230-331-22
; Sequence 22, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-230-331-22

Query Match      51.0%; Score 74; DB 14; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 15
US-10-408-765A-2109
; Sequence 2109, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2109
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2109

Query Match      51.0%; Score 74; DB 16; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0062;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPDYEFSAPEYISQINEIXYT 28
   |||||:::|||||:::
Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 16
US-10-230-331-25
; Sequence 25, Application US/10230331

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; TYPE: PRF
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-75

Query Match      48.3%; Score 70; DB 15; Length 214;
Best Local Similarity   61.9%; Pred.No. 0.024;
Matches    13; Conservative     3; Mismatches     5; Indels     0; Gaps     0;

QY       2 YSLPELDYEFSAEPIYSIGOI 22
          ||||| |: | ||| :|
Db        13 YSLPELPDYDALEPVISSRI 33

RESULT 19
US-10-230-331-24
; Sequence 24, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTIC CELLS
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 233
; TYPE: PRF
; ORGANISM: Pisum sativum
US-10-230-331-24

Query Match      48.3%; Score 70; DB 14; Length 233;
Best Local Similarity   46.2%; Pred.No. 0.026;
Matches    12; Conservative     8; Mismatches     6; Indels     0; Gaps     0;

QY       2 YSLPELDYEFSAEPIYSGINEIXY 27
          ::||:||::|||:|||:||:|
Db        40 FTPLDLYDAYLEPVISGEIMQH 65

RESULT 20
US-10-156-761-12947
; Sequence 12947, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12947
; LENGTH: 213
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12947

Query Match      46.9%; Score 68; DB 14; Length 213;
Best Local Similarity   50.0%; Pred.No. 0.047;
Matches    13; Conservative     6; Mismatches     7; Indels     0; Gaps     0;
```

RESULT 22

US-10-310-154-662

Sequence 662, Application US/10310154

Publication No. US20023670A1

GENERAL INFORMATION:

APPLICANT: EGGERTON, Michael D

APPLICANT: Chomet, Paul S.

APPLICANT: Adams, Thomas H

APPLICANT: Ruff, Thomas G.

APPLICANT: Agarwal, Ameta K.

APPLICANT: Ahrens, Jeffrey E.

APPLICANT: Ball, James A.

APPLICANT: Banu, G.

APPLICANT: Bell, Erin

APPLICANT: Boddupalli, Raghava

APPLICANT: Deikman, Jill

APPLICANT: Deng, Jolian

APPLICANT: Dong, Jizhuo

APPLICANT: Duff, Stephen M.

APPLICANT: Galligan, Meghan M.

APPLICANT: Hinchey, Brenda S.

APPLICANT: Huang, Shihshieh

APPLICANT: Johnson, G. Richard

APPLICANT: Jung, Vincent

APPLICANT: Kretzmer, Keith A

APPLICANT: Laccetti, Lucille B.

APPLICANT: Lai, Chao-Qiang

APPLICANT: Lee, Gary

APPLICANT: Lin, Jie-Yi

APPLICANT: Liu, Jingdong

APPLICANT: Lu, Bin

APPLICANT: Luethy, Michael M.

APPLICANT: Lund, Adrian

APPLICANT: Magson, Linda L.

APPLICANT: Malloy, Kathleen A.

APPLICANT: McKiel, Christine L.

APPLICANT: Miller, Philip W.

APPLICANT: Padmavathi, Manichakanti

RESULT 24
US-09-953-510-23
; Sequence 23, Application US/09953510
; Patent No. US20020131975A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Products
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
;


```

; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,510
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
; US-09-953-510-23
;
; Query Match 45.5%; Score 66; DB 9; Length 22;
; Best Local Similarity 61.1%; Pred. No. 0.0073;
; Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
; QY 4 LPELDYEFSATEPYISGQ 21
; Db 5 LPDLWDYGALEPHISGQ 22
;
; RESULT 25
; US-09-953-413-23
; Sequence 23, Application US/09953413
; Publication No. US20040018209A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,413
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MacLean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
; US-09-953-413-23
;
; Query Match 45.5%; Score 66; DB 11; Length 22;
; Best Local Similarity 61.1%; Pred. No. 0.0073;
; Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
;
; QY 4 LPELDYEFSATEPYISGQ 21
; Db 5 LPDLWDYGALEPHISGQ 22
;
; RESULT 26
; US-10-147-255-23
; Sequence 23, Application US/10147255
; Publication No. US20030152584A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. MacLean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/226,539A
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: US 08/447,398
;; FILING DATE: 23-MAY-1995
;; APPLICATION NUMBER: US 08/289,667
;; FILING DATE: 12-AUG-1994
;; APPLICATION NUMBER: US 08/156,359
;; FILING DATE: 23-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MacLean, Kurt A.
;; REGISTRATION NUMBER: 31,118
;; REFERENCE/DOCKET NUMBER: 112-272
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (310) 788-5000
;; TELEFAX: (310) 277-1297
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEetical: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Mycobacterium tuberculosis
;; STRAIN: Erdman
;; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-147-255-23

Query Match 45.5%; Score 66; DB 14; Length 22;
Best Local Similarity 61.1%; Pred. No. 0.0073;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LPDLDFEFSATEPYISQ 21
Db 5 LPDLWDYGALEPHISQ 22

RESULT 27
US-09-727-855B-5
; Sequence 5, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOCIDS AND BIOLOGICALLY USEFUL
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-5

Query Match 45.5%; Score 66; DB 9; Length 222;
Best Local Similarity 46.4%; Pred. No. 0.098;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KYSLPDLDFEFSATEPYISQINEIXT 28
Db 26 KHTLPDLPAYDALEPSISKELMILHT 53

RESULT 28
US-10-424-599-184874

;; Sequence 184874, Application US/10424599
;; Publication No. US20040031072A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa Thomas J
;; APPLICANT: Kovalic David K
;; APPLICANT: Zhou Yihua
;; APPLICANT: Cao Yongwei
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US/10/424,599
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 184874
;; LENGTH: 80
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1)..(80)
;; OTHER INFORMATION: unsure at all Xaa locations
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT MRT3847_137957C.1.pap
US-10-424-599-184874

Query Match 44.8%; Score 65; DB 12; Length 80;
Best Local Similarity 42.3%; Pred. No. 0.044;
Matches 11; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 YSLPDLDFEFSATEPYISQINEIXY 27
Db 32 YTLPLDLDYDXALEPAXSXDIQMLHH 57

RESULT 29
US-10-230-331-27
; Sequence 27, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTE
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ganoderma microsporum
US-10-230-331-27

Query Match 44.8%; Score 65; DB 14; Length 200;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 4 LPDLDFEFSATEPYISQINEIXY 27
Db 5 LPDLPAYNALEPFISQIMELHH 28

RESULT 30
US-10-109-670-10
; Sequence 10, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01

201 EFPMPVLA YKFSVTDP-ISGO 220

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RESULT 38
US-10-369-493-6225
; Sequence 6225, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6225
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6225

Query Match      35.9%; Score 52; DB 15; Length 633;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      5 PELDYFESATEPYISQI 22
       |:|:|:|:|:|:|:|:|:|
Db      356 PQLDYDFGTETPTRIQKI 373

RESULT 39
US-10-437-963-163657
; Sequence 163657, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163657
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62632C.1.pep
US-10-437-963-163657

Query Match      35.5%; Score 51.5; DB 16; Length 384;
Best Local Similarity 55.0%; Pred. No. 28;
Matches 11; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY      2 YSLPELDYFESATEPYISQ 21
       : :|:|:|:|:|:|:|:|:|
Db      330 FPMPLVLYKFSVTDP-ISGQ 348

RESULT 40
US-10-437-963-163658
; Sequence 163658, Application US/10437963
```

```
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163658
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(770)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62633C.1.pep
US-10-437-963-163658

Query Match      35.5%; Score 51.5; DB 16; Length 770;
Best Local Similarity 55.0%; Pred. No. 60;
Matches 11; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY      2 YSLPELDYFESATEPYISQ 21
       : :|:|:|:|:|:|:|:|:|
Db      716 FPMPLVLYKFSVTDP-ISGQ 734

Search completed: August 24, 2004, 23:13:35
Job time : 125 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 22:48:16 ; Search time 23 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-09-987-190-2
Perfect score: 145
Sequence: 1 KYSLPELYRFSATEPYISQINEIXYTX 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	141	97.2	234	1 SODM_CANAL	O13401 candida alb
2	103	71.0	206	1 SODM_NOCAS	P53651 nocardia as
3	101	69.7	206	1 SODM_MYCAV	P47201 mycobacteri
4	100	69.0	206	1 SODM_MYCLP	O86165 mycobacteri
5	100	69.0	233	1 SODM_YEAST	P00447 saccharomyc
6	99	68.3	206	1 SODM_MYCFO	Q59519 mycobacteri
7	98	68.3	206	1 SODM_MYCSM	P53649 mycobacteri
8	98	67.6	206	1 SODM_MYCLE	P13367 mycobacteri
9	94	64.8	207	1 SODF_MYCTU	P17670 mycobacteri
10	91	62.8	201	1 SODM_PROFR	P80293 propionibac
11	83	57.2	245	1 SODM_NEUCR	Q9Y783 nektospora
12	80	55.2	222	1 SODM_HORSE	Q9X841 equus caball
13	78	53.8	199	1 SODM_CORDI	P42821 corynebacte
14	77	53.1	202	1 SODM_RABIT	P41982 oryctolagus
15	76	52.4	202	1 SODF_METJ	P23744 methylomona
16	74	52.0	198	1 SODM_CALJA	Q8bhp0 callithrix
17	74	51.0	198	1 SODM_CBPAP	Q8bhp1 cebus apell
18	74	51.0	198	1 SODM_HYLLA	Q8bhp5 hylobates l
19	74	51.0	198	1 SODM_MACFA	Q8bhp3 macaca fasc
20	74	51.0	198	1 SODM_MACFU	Q8bhp4 macaca fusc
21	74	51.0	198	1 SODM_PANTR	Q8bhp2 macaca mula
22	74	51.0	198	1 SODM_PANTR	Q8bhp7 pan troglod
23	74	51.0	198	1 SODM_PONPY	Q8bhp6 pongo pygma
24	74	51.0	211	1 SODF_ACIAM	Q9P913 acidiarius a
25	74	51.0	222	1 SODM_BOVIN	P41976 bos taurus
26	74	51.0	222	1 SODM_HUMAN	P04179 homo sapien
27	74	51.0	222	1 SODM_MOUSE	P09571 mus musculu
28	74	51.0	222	1 SODM_RAT	P07895 rattus norv
29	73	50.3	210	1 SODF_SULSO	P80857 sulfolobus
30	72	49.7	211	1 SODF_PYRAE	Q93724 pyrobaculum
31	72	49.7	228	1 SODM_CAPAN	Q94066 capsicum an
32	71	49.0	210	1 SODM_ASFPU	Q92450 aspergillus
33	71	49.0	233	1 SODM_HEVBR	P35017 hevea bras

RESULT 1

ID	SODM_CANAL	STANDARD;	PRT;	234 AA.
AC	O13401;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).			
GN	SOD2			
OS	Candida albicans (Yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Mitosporic Saccharomycetales; Candida.			
OX	NCBI_TaxID=5476;			
RN	[1]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.			
RX	MEDLINE=99177433; PubMed=10076057;			
RA	Rhie G.E., Hwang C.S., Brady M.J., Kim S.T., Kim Y.R., Huh W.K.,			
RA	Baek Y.U., Lee B.H., Lee J.S., Kang S.O.;			
RT	"Manganese-containing superoxide dismutase and its gene from Candida albicans";			
RL	Biochim. Biophys. Acta 1426:409-419(1999).			
CC	-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.			
CC	-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).			
CC	-!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).			
CC	-!- SUBUNIT: Homotetramer.			
CC	-!- SUBCELLULAR LOCATION: Mitochondrial matrix.			
CC	-!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: AF031478; AAB85893.1; --			
DR	HSSP; P04179; IABM.			
DR	InterPro; IPR001189; SODismutase.			
DR	Pfam; PF00081; sodfe; 1.			
DR	Pfam; PF02777; sodfe.C; 1.			
DR	PRINTS; PR01703; MNSODISMUTASE.			
DR	ProDom; PD000475; SODismutase; 1.			
DR	PROSITE; PS00088; SOD_MN; 1.			
KW	Oxidoreductase; Metal-binding; Manganese; Mitochondrion;			
FT	Transit peptide.			
FT	TRANSIT 1 34 MITOCHONDRION.			
FT	CHAIN 35 234 SUPEROXIDE DISMUTASE [MN].			
FT	METAL 60 60 MANGANESE (BY SIMILARITY).			
FT	METAL 108 108 MANGANESE (BY SIMILARITY).			
FT	METAL 198 198 MANGANESE (BY SIMILARITY).			
FT	METAL 202 202 MANGANESE (BY SIMILARITY).			
SQ	SEQUENCE 234 AA; 26173 MW; EBFEC2D769C1D9C1 CRC64;			

ALIGNMENTS

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P47201; AC
01-FEB-1996 (Rel. 33, Created) DT
01-OCT-1996 (Rel. 34, Last sequence update) DT
10-OCT-2003 (Rel. 42, Last annotation update) DE
Superoxide dismutase [Mn] (EC 1.15.1.1). DE
SODA OR SOD. GN
Mycobacterium avium. OS
Bacteria; Actinobacteria; Actinomycetales; OC
Corynebacteriaceae; Mycobacteriaceae; MYCOBACTERIUM. OC
NCBI_TaxID=1784; OX
[1] RN
SEQUENCE FROM N.A. RP
STRAIN=TMC 724; RX
MEDLINE=96276149; PubMed=8692009; RA
Escuyer V.E., Haddad N., Frehel C., Berche P.; RT
"Molecular characterization of a surface-exposed superoxide dismutase of Mycobacterium avium."; RL
Microb. Pathog. 20:41-55(1996). RC
CC -! FUNCTION: Destroys radicals which are normally produced within the CC
cells and which are toxic to biological systems. CC
-! CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2). CC
-! COFACTOR: Binds 1 manganese ion per subunit (By similarity). CC
-! SIMILARITY: Belongs to the iron/manganese superoxide dismutase CC
family. CC
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EMBL; U11550; AAB08770.1; -- DR
HSP; P17670; LIDS. DR
InterPro; IPR001189; SODismutase. DR
Pfam; PF00081; sodefr_1. DR
pfam; PF02777; sodefr_C; 1. DR
PRINTS; PR01703; MNSDISMTASE. DR
ProDom; PD000475; SODISMutase; 1. DR
PROSITE; PS00088; SOD MN; 1. DR
OXidoreductase; Metal-binding; Manganese. KW
INIT_MET 0 BY SIMILARITY. FT
METAL 27 27 MANGANESE (BY SIMILARITY). FT
METAL 75 75 MANGANESE (BY SIMILARITY). FT
METAL 159 159 MANGANESE (BY SIMILARITY). FT
METAL 163 163 MANGANESE (BY SIMILARITY). FT
SEQUENCE 206 AA; 22912 MW; D6B49083AEBF3C98 CRC64; SQ
Query Match 69.7%; Score 101; DB 1; Length 206;
Best Local Similarity 60.7%; Pred.No. 9e-08; Gaps 0;
Matches 17; Conservative 9; Mismatches 2; Indels 0;
QY 1 KYSLPELDVFSATEPVYSQGINEIXYT 28
:|:||||::||::||::||||||:|
DB 2 EYTEPLDWDYALEPHISGQINEIHHT 29
:|:||||::||::||::||||||:|
RESULT 4
SODM_MYCLP STANDARD; PRT; 206 AA. ID_SODM_MYCLP
AC Q861K5; AC
30-MAY-2000 (Rel. 39, Created) DT
30-MAY-2000 (Rel. 39, last sequence update) DT
DT 10-OCT-2003 (Rel. 42, Last annotation update) DE
Superoxide dismutase [Mn] (EC 1.15.1.1). DE
SODA OR SOD. GN
Mycobacterium lepraeurum. OS
Bacteria; Actinobacteria; Actinomycetales; OC
Corynebacteriaceae; Mycobacteriaceae; MYCOBACTERIUM. OC
NCBI_TaxID=64667; OX
[1] RN
SEQUENCE FROM N.A. RP

```


RC STRAIN=Hawaiian;
 RA Nakamura M.;
 RL Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 CC
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 CC
 CC EMBL; D13288; BAA28850.1; -;
 DR HSSP; P17670; IIDS.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese.
 FT INIT MET 0 BY SIMILARITY.
 FT METAL 27 27 MANGANESE (BY SIMILARITY).
 FT METAL 75 75 MANGANESE (BY SIMILARITY).
 FT METAL 159 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 206 AA; 23031 MW; 92A063471FA9F22F CRC64;
 Query Match 69.0%; Score 100; DB 1; Length 206;
 Best Local Similarity 60.7%; Pred. No. 1.3e-07;
 Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KYSLPELDYEFSAPEYISQGINEIXYT 28
 DB 2 EYLPDLWDYEALEPHISQGINEIHT 29
 RESULT 5
 SODM YEAST
 ID SODM YEAST STANDARD; PRT; 233 AA.
 AC P00447;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2 OR YHR008C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85127011; PubMed=3882422;
 RA Marras C.A.M., van Loon A.P.G.M., Oudshoorn P., van Steeg H.,
 RA Grivell L.A., Slater E.C.;
 RA "Nucleotide sequence analysis of the nuclear gene coding for
 RT manganese superoxide dismutase of yeast mitochondria, a gene
 RT previously assumed to code for the Rieske iron-sulphur protein.";
 RL Eur. J. Biochem. 147:153-161(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,

RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII.";
 RL Science 265:2077-2082(1994).
 RN [3]
 RP SEQUENCE OF 1-39 FROM N.A.
 RX MEDLINE=89211942; PubMed=3072251;
 RA Schrank I.S., Sims P.F., Oliver S.G.;
 RT "Functional expression of the yeast Mn-superoxide dismutase gene in
 RT Escherichia coli requires deletion of the signal peptide sequence.";
 RL Gene 73:121-130(1988).
 RN [4]
 RP SEQUENCE OF 27-233.
 RX MEDLINE=9211942; PubMed=3072251;
 RA Schrank I.S., Sims P.F., Oliver S.G.;
 RT "Functional expression of the yeast Mn-superoxide dismutase gene in
 RT Escherichia coli requires deletion of the signal peptide sequence.";
 RL Gene 73:121-130(1988).
 RN [4]
 RP SEQUENCE OF 27-233.
 RA Ditlow C., Johansen J.T., Martin B.M., Svendsen I.;
 RT "The complete amino acid sequence of manganese-superoxide dismutase
 RT from Saccharomyces cerevisiae.";
 RL Carlsberg Res. Commun. 47:81-91(1982).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 CC
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 CC
 CC EMBL; X02156; CAA26092.1; -;
 DR EMBL; U10400; AAB88939.1; -;
 DR EMBL; M24079; AAA35065.1; -;
 DR FIR; A00521; DSBYN.
 DR HSSP; P04179; IABM.
 DR GermOnline; 139325; -;
 DR SGD; S0001050; SOD2.
 DR GO; GO:0005759; C:mitochondrial matrix; IDA.
 DR GO; GO:0008383; F:manganese superoxide dismutase activity; IDA.
 DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IMP.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 KW Transit peptide.
 FT TRANSIT 1 26 MITOCHONDRION
 FT CHAIN 27 233 SUPEROXIDE DISMUTASE [MN].
 FT METAL 52 52 MANGANESE (BY SIMILARITY).
 FT METAL 107 107 MANGANESE (BY SIMILARITY).
 FT METAL 194 194 MANGANESE (BY SIMILARITY).
 FT METAL 198 198 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 233 AA; 25774 MW; 88A9391FBB31D06E CRC64;
 Query Match 69.0%; Score 100; DB 1; Length 233;
 Best Local Similarity 64.3%; Pred. No. 1.4e-07;
 Matches 18; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KYSLPELDYEFSAPEYISQGINEIXYT 28
 DB 27 KVTLPDLKWDYEALEPHISQGINEIHT 54
 RESULT 6
 SODM_MYCFO

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ID SODM_MYCFO STANDARD; PRT; 206 AA.
AC Q59519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.
OS Mycobacterium fortuitum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1766;

[1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP STRAIN=1-2C;
RX MEDLINE=99134360; PubMed=9933629;
RA Harth G., Horwitz M.A.;
RT "Export of recombinant Mycobacterium tuberculosis superoxide dismutase
is dependent upon both information in the protein and mycobacterial
export machinery. A model for studying export of leaderless proteins
by pathogenic mycobacteria.";
RL J. Biol. Chem. 274:4281-4292(1999).

[2]
RN REVISIONS TO 116 AND 201.
RP Tullius M.V., Harth G., Horwitz M.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

[3]
RN SEQUENCE OF 27-164 FROM N.A.
RP STRAIN=NCTC 10265 / ATCC 14468 / W-113;
RX Bull T.J., Shanson D.C., Archard L.C.;
RA "Rapid identification of mycobacteria from AIDS patients by capillary
RT electrophoretic profiling of amplified SOD gene.";
RL J. Clin. Pathol. Clin. Mol. Pathol. 48:124-132(1995).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.

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CC -----
DR EMBL; X70914; CAA50266.1; -.
DR PIR; S60669; S60669.
DR HSP; P17670; LIDS.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
DR Oxidoreductase; Metal_binding; Manganese.
KW INIT_MET 0 BY SIMILARITY.
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 75 75 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 206 AA; 22833 MW; 500625A8B9321246 CRC64;

Query Match 68.3%; Score 99; DB 1; Length 206;
Best Local Similarity 57.1%; Pred. No. 1.8e-07;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KYSLPELDYEFSAPEYISQINIEYXT 28
Db 2 EYTLPLDLDYDYGALPHISQINELHHS 29

RESULT 7
SODM_MYCSM STANDARD; PRT; 206 AA.
AC P53649; Q9S612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;

[1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP STRAIN=ATCC 6841;
RX MEDLINE=96102872; PubMed=8586279;
RA Menendez M.C., Domenech P., Prieto J., Garcia M.J.;
RT "Cloning and expression of the Mycobacterium fortuitum superoxide
dismutase gene.";
RL FEMS Microbiol. Lett. 134:273-278(1995).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.

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CC -----
DR EMBL; X70914; CAA50266.1; -.
DR PIR; S60669; S60669.
DR HSP; P17670; LIDS.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
DR Oxidoreductase; Metal_binding; Manganese.
KW INIT_MET 0 BY SIMILARITY.
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 75 75 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 206 AA; 22833 MW; 500625A8B9321246 CRC64;

Query Match 68.3%; Score 99; DB 1; Length 206;
Best Local Similarity 57.1%; Pred. No. 1.8e-07;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KYSLPELDYEFSAPEYISQINIEYXT 28
Db 2 EYTLPLDLDYDYGALPHISQINELHHS 29

RESULT 8
SODM_MYCLE STANDARD; PRT; 206 AA.
AC P13367;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).

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FT	METAL	28	28	IRON.
FT	METAL	76	76	IRON.
FT	METAL	160	160	IRON.
FT	METAL	164	164	IRON.
FT	TURN	13	19	
FT	HELIX	22	30	
FT	TURN	31	31	
FT	HELIX	32	52	
FT	TURN	53	54	
FT	TURN	57	58	
FT	HELIX	59	82	
FT	STRAND	83	83	
FT	TURN	85	86	
FT	HELIX	93	103	
FT	HELIX	106	118	
FT	STRAND	124	131	
FT	TURN	132	135	
FT	STRAND	136	143	
FT	TURN	144	146	
FT	STRAND	147	147	
FT	TURN	151	152	
FT	STRAND	153	160	
FT	HELIX	163	165	
FT	TURN	166	166	
FT	HELIX	167	170	
FT	TURN	171	172	
FT	HELIX	174	180	
FT	HELIX	181	183	
FT	STRAND	185	185	
FT	HELIX	187	198	
SQ	SEQUENCE	207 AA;	23034 MW; DEE8F5921DABE5A4 CRC64;	

Query Match 64.8%; Score 94; DB 1; Length 207;
Best Local Similarity 53.6%; Pred. No. 1e-06;
Matches 15; Conservative 10; Mismatches 3; Indels 0

OY	1 KYSIPELDYERSNTEPYISGOINELXYT 28 : ::: : :::
DB	3 EYTLPLDWYDYGALPHISGQINELHHS 30 : ::: : :::

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RESULT 10
SODM_PROPR
ID SODM_PROFR STANDARD; PRT; 201 AA.
AC F80293;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
GN SODA
OS Propionibacterium freudenreichii shermanii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1752;
RN [1]
RP SEQUENCE.
RC STRAIN=EZ3;
RX MEDLINE=94139724; PubMed=8307013;
RA Meier B., Sehn A.P., Schinina M.E., Barra D.;
RT "In vivo incorporation of copper into the iron-exchangeable a-
RT manganese-exchangeable superoxide dismutase from Propionibact-
RT ermanii. Amino acid sequence and identity of the protein
RT moieties."
RL Eur. J. Biochem. 219:463-468(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RA Schmidt M., Meier B., Parak F.;
RT "X-ray structure of the cambialistic superoxide dismutase from
RT Propionibacterium shermanii active with Fe or Mn."
RJ J. Biol. Inorg. Chem. 1:532-541(1996).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RA Schmidt M., Scherk C., Iakovleva O., Nolling H.F., Meier B.,

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RL Submitted (SEP-1997) to the PDB data bank.
RP [4]
RX X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
RA MEDLINE=99248073; PubMed=10231372;
RA Schmidt M.;
RT "Manipulating the coordination number of the ferric iron within the
RT cambialistic superoxide dismutase of Propionibacterium shermanii by
RT changing the pH-value. A crystallographic analysis."
RL Eur. J. Biochem. 262:117-127(1999).
CC -I- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -I- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -I- COFACTOR: Binds 1 manganese or iron ion per subunit.
CC -I- SUBUNIT: Homotetramer.
CC -I- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR PIR; JC4396.
DR PDB; 1AR4; 12-NOV-97.
DR PDB; 1AR5; 12-NOV-97.
DR PDB; 1AVM; 18-MAR-98.
DR PDB; 1BS3; 15-JUN-99.
DR PDB; 1BSN; 15-JUN-99.
DR PDB; 1BT8; 15-JUN-99.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF000081; sodfe; 1.
DR Pfam; PF02777; sodfe; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR PROSITE; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Iron; 3D-structure.
FT METAL 27 27
FT METAL 75 75 MANGANESE OR IRON.
FT METAL 161 161 MANGANESE OR IRON.
FT METAL 165 165 MANGANESE OR IRON.
FT TURN 12 18
FT HELIX 21 29
FT TURN 30 30
FT HELIX 31 52
FT TURN 53 53
FT TURN 55 57
FT HELIX 58 80
FT TURN 81 81
FT STRAND 82 82
FT TURN 85 86
FT HELIX 94 104
FT HELIX 107 119
FT TURN 120 120
FT STRAND 125 132
FT TURN 133 136
FT STRAND 137 144
FT TURN 145 147
FT STRAND 148 148
FT TURN 152 153
FT STRAND 155 161
FT HELIX 164 166
FT TURN 167 167
FT HELIX 168 171
FT TURN 172 173
FT HELIX 175 182
FT STRAND 183 185
FT HELIX 186 186
FT STRAND 188 198
FT TURN 199 199
SQ SEQUENCE 201 AA; 22633 MW; 5BFF424C7B32E00 CRC64;

Query Match 62.8%; Score 91; DB 1; Length 201;
Best Local Similarity 61.5%; Pred. No. 2.7e-06;
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 YSLPELDVEFSATEPYISQINEIXY 27
DB 3 YTLPELDYDYSALEPYISQINEIMELH 28

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RESULT 11
SODM_NEUCR
ID _SODM_NEUCR STANDARD; PRT; 245 AA.
AC Q9Y783;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (RC 1.15.1.1).
GN SOD-2 OR 18F11.030.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
SEQUENCE FROM N.A.
RP Dvorachek W.H., Natvig D.N.;
RA "Characterization of sod-2, the Neurospora crassa gene for manganese
RT superoxide dismutase."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22542210; PubMed=12655011;
RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
RA Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
RA Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the
RT Neurospora genome sequence."
RL Nucleic Acids Res. 31:1944-1954(2003).
CC -I- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -I- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -I- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -I- SUBUNIT: Homotetramer (By similarity).
CC -I- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -I- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
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EMBL; AF118809; AAD28503.1; -.
DR EMBL; AL670011; CAD21408.1; -.
DR HSSP; P04179; 1AEM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF000081; sodfe; 1.
DR Pfam; PF02777; sodfe; C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 32 MITOCHONDRION (POTENTIAL).
FT CHAIN 33 245 SUPEROXIDE DISMUTASE [MN].
FT METAL 58 58 MANGANESE (BY SIMILARITY).
FT METAL 106 106 MANGANESE (BY SIMILARITY).
FT METAL 196 196 MANGANESE (BY SIMILARITY).
FT METAL 200 200 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 245 AA; 27019 MW; FF288947FB7676AD CRC64;

Query Match 57.2%; Score 83; DB 1; Length 245;
Best Local Similarity 55.6%; Pred. No. 5.2e-05;
Matches 15; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDVEFSATEPYISQINEIXY 28
DB 34 YSLPOLPAYNALEPYISQIMELHHS 60

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RESULT 12
SODM_HORSE
ID _SODM_HORSE STANDARD; PRT; 222 AA.
AC Q9XS41
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
DE (Mn-SOD).
GN SOD2
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RX MEDLINE=99261591; PubMed=10331206;
RA Ishida N., Katayama Y., Sato F., Hasegawa T., Mukoyama H.;
RT "The cDNA sequences of equine antioxidant enzyme genes Cu/Zn-SOD and
Mn-SOD, and these expressions in equine tissues.";
J. Vet. Med. Sci. 61:291-294(1999).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
-----
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-----
EMBL; AB001693; BAA76922.1; --
HSSP; P04179; IABM.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
PRINTS; PR01703; MNSODISMUTASE.
ProDom; PD000475; SODismutase; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
Transit peptide.
KW TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).
FT METAL 98 98 MANGANESE (BY SIMILARITY).
FT METAL 183 183 MANGANESE (BY SIMILARITY).
FT METAL 187 187 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 222 AA; 24739 MW; 93A069481944E98C CRC64;

Query Match 55.2%; Score 80; DB 1; Length 222;
Best Local Similarity 46.4%; Pred. No. 0.00013;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFSGATEPYISGQINEIXYT 28
Db 25 KHSLPDLQYDYGALEPYINQIMQLHHS 52

RESULT 13
SODM_CORDI
ID _SODM_CORDI STANDARD; PRT; 199 AA.
AC P42821;
DT 01-NOV-1995 (Rel. 32, Created)

Query Match 53.8%; Score 78; DB 1; Length 199;
Best Local Similarity 48.1%; Pred. No. 0.00023;
Matches 13; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSGATEPYISGQINEIXYT 28
Db 3 YALPELDYADALEPHTAAEIMELHHS 29
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DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).
GN SODA OR SOD OR DIF261.
OS Corynebacterium diptheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Biotype gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910;
RA Cerdeno-Tarraga A.M., Efstathiou A., Dover L.G., Holden M.T.G.,
Pallen M., Bentley S.D., Besra G.S., Churcher C., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Jegeris K., Moule S., Quail M.A.,
Rabinowitz B., Rutherford K.M., Thomson N.R., Unwin L.,
Whitehead S., Barrell B.G., Parkhill J.;
RT "The complete genome sequence and analysis of Corynebacterium
diptheriae NCTC13129.";
Nucleic Acids Res. 31:6516-6523(2003).
[2]
RN SEQUENCE OF 26-189 FROM N.A.
RP STRAIN=ATCC 11913;
RX MEDLINE=95155602; PubMed=7852575;
RA Zolg J.W., Philipp-Schulz S.;
RT "The superoxide dismutase gene, a target for detection and
identification of mycobacteria by PCR.";
J. Clin. Microbiol. 32:2801-2812(1994).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
-----
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-----
EMBL; BX248360; CAB50785.1; --
EMBL; X81382; CAA57145.1; --
PIR; I40677; I40677.
HSSP; P17670; LIIDS.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
PRINTS; PR01703; MNSODISMUTASE.
ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD_MN; 1.
Oxidoreductase; Metal-binding; Manganese.
FT METAL 28 28 MANGANESE (BY SIMILARITY).
FT METAL 76 76 MANGANESE (BY SIMILARITY).
FT METAL 160 160 MANGANESE (BY SIMILARITY).
FT METAL 164 164 MANGANESE (BY SIMILARITY).
FT CONFLICT 41 41 A -> T (IN REF. 2).
FT CONFLICT 123 124 MISSING (IN REF. 2).
FT CONFLICT 185 185 F -> V (IN REF. 2).
SQ SEQUENCE 199 AA; 21886 MW; AAAB70FF509078D8 CRC64;

Query Match 53.8%; Score 78; DB 1; Length 199;
Best Local Similarity 48.1%; Pred. No. 0.00023;
Matches 13; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 YSLPELDYFSGATEPYISGQINEIXYT 28
Db 3 YALPELDYADALEPHTAAEIMELHHS 29
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RESULT 14
SODM RABIT
ID SODM RABIT STANDARD; PRT; 202 AA.
AC P41982;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
DE (Fragment).
DE
DE
GN SOD2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RA Jackson R.M.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L28808; AAA31401.1; -.
DR HSSP; P04179; 1AP6.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT NON_TER 1 5 MITOCHONDRION (BY SIMILARITY).
FT TRANSIT <1 5
FT CHAIN 6 >202 SUPEROXIDE DISMUTASE [MN].
FT METAL 31 31 MANGANESE (BY SIMILARITY).
FT METAL 79 79 MANGANESE (BY SIMILARITY).
FT METAL 164 164 MANGANESE (BY SIMILARITY).
FT METAL 168 168 MANGANESE (BY SIMILARITY).
FT NON_TER 202 202
SQ SEQUENCE 202 AA; 22656 MW; 6F1BB8DA15C33AA7 CRC64;

Query Match 53.1%; Score 77; DB 1; Length 202;
Best Local Similarity 46.4%; Pred. No. 0.00033;
Matches 13; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAATEPVYISGQINEIXYT 28
DB 6 KHSPLDPLDYGALEPHINAQIMELHHS 33

RESULT 15
SODF METU
ID SODF METU STANDARD; PRT; 202 AA.
AC P23744;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
DE

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GN SODB.
OS Methylobacter J.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylobacter.
OX NCBI_TaxID=32038;
RN [1]
RN
RP SEQUENCE.
RX MEDLINE=91182736; PubMed=1848999;
RA Matsumoto T., Terauchi K., Isobe T., Matsuo K., Yamakura F.;
RT "Iron- and manganese-containing superoxide dismutases from
RT Methylobacter J.: identity of the protein moiety and amino acid
RT sequence."
RL Biochemistry 30:3210-3216 (1991).
RN [2]
RN
RP CHARACTERIZATION, AND SEQUENCE OF 1-32.
RX MEDLINE=91301511; PubMed=1906419;
RA Yamakura F., Matsumoto T., Terauchi K.;
RT "Isolation of Mn-SOD and low active Fe-SOD from Methylobacter J.
RT consisting of identical proteins."
RL Free Radic. Res. Commun. 12:329-334 (1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese or iron ion per subunit (By
CC similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
CC HSSP; P00448; 1VEW.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Iron.
FT METAL 26 26 MANGANESE OR IRON (BY SIMILARITY).
FT METAL 80 80 MANGANESE OR IRON (BY SIMILARITY).
FT METAL 163 163 MANGANESE OR IRON (BY SIMILARITY).
FT METAL 167 167 MANGANESE OR IRON (BY SIMILARITY).
SQ SEQUENCE 202 AA; 22363 MW; 3213A8B4697A5B58 CRC64;

Query Match 52.4%; Score 76; DB 1; Length 202;
Best Local Similarity 51.9%; Pred. No. 0.00047;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATEPVYISGQINEIXYT 28
DB 2 YLPLDLYATYALEPHIDAQTWEIHT 28

RESULT 16
SODM CALJA
ID SODM CALJA STANDARD; PRT; 198 AA.
AC Q8HYE0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases."
RL Gene 296:99-109 (2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the

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CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC
CC EMBL: AB087281; BAC20360.1; ALT_INIT.
CC InterPro: IPR001189; SODismutase.
CC Pfam: PF00081; sodfe; 1.
CC PRINTS: PR01703; MNSODISMUTASE.
CC PRODOM: PD000475; SODismutase; 1.
CC OXIDOREDUCTASE: Metal-binding; Manganese; Mitochondrion.
CC METAL 26 26 MANGANESE (BY SIMILARITY).
CC METAL 74 74 MANGANESE (BY SIMILARITY).
CC METAL 159 159 MANGANESE (BY SIMILARITY).
CC METAL 163 163 MANGANESE (BY SIMILARITY).
CC SEQUENCE 198 AA; 22248 MW; E7F860B8C56F2CA CRC64;
CC
CC Query Match 51.0%; Score 74; DB 1; Length 198;
CC Best Local Similarity 42.9%; Pred. No. 0.0009;
CC Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 1 KYSLPELDYFSAPEYISQINEIXYT 28
CC Db 1 KHSLPDLPDYGALEPHINQMQLHHS 28
CC
CC RESULT 18
CC SODM_HYLLA STANDARD; PRT; 198 AA.
CC ID SODM_HYLLA STANDARD; PRT; 198 AA.
CC AC Q8HXP5;
CC DT 15-MAR-2004 (Rel. 43, Created)
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
CC GN SOD2.
CC OS Hylobates lar (Common gibbon).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
CC OX NCBI_TaxID=9580;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=2271545; PubMed=12383507;
CC RA Fukuhara R., Tezuka T., Kageyama T.;
CC RT "Structure, molecular evolution, and gene expression of primate
CC RT superoxide dismutases."
CC RL Gene 296:99-109(2002).
CC CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC CC cells and which are toxic to biological systems.
CC CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC CC -!- SUBUNIT: Homotetramer (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC CC family.
CC
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CC
CC EMBL: AB087276; BAC20355.1; ALT_INIT.
CC InterPro: IPR001189; SODismutase.
CC Pfam: PF00081; sodfe; 1.
CC PRINTS: PR01703; MNSODISMUTASE.
CC PRODOM: PD000475; SODismutase; 1.
CC OXIDOREDUCTASE: Metal-binding; Manganese; Mitochondrion.
CC METAL 26 26 MANGANESE (BY SIMILARITY).
CC METAL 74 74 MANGANESE (BY SIMILARITY).
CC SEQUENCE 198 AA; 22248 MW; E7F860B8C56F2CA CRC64;
CC
CC Query Match 51.0%; Score 74; DB 1; Length 198;
CC Best Local Similarity 42.9%; Pred. No. 0.0009;
CC Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 1 KYSLPELDYFSAPEYISQINEIXYT 28
CC Db 1 KHSLPDLPDYGALEPHINQMQLHHS 28
CC
CC RESULT 17
CC SODM_CEBAP STANDARD; PRT; 198 AA.
CC ID SODM_CEBAP STANDARD; PRT; 198 AA.
CC AC Q8HXP1;
CC DT 15-MAR-2004 (Rel. 43, Created)
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
CC GN SOD2.
CC OS Cebus apella (Brown-capped capuchin).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
CC OX NCBI_TaxID=9515;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=2271545; PubMed=12383507;
CC RA Fukuhara R., Tezuka T., Kageyama T.;
CC RT "Structure, molecular evolution, and gene expression of primate
CC RT superoxide dismutases."
CC RL Gene 296:99-109(2002).
CC CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC CC cells and which are toxic to biological systems.
CC CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC CC -!- SUBUNIT: Homotetramer (By similarity).
CC CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC CC family.
CC
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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SQ SEQUENCE      211 AA;   24342 MW;  5A88FFE400F77065 CRC64;

Query Match          51.0%; Score 74; DB 1; Length 211;
Best Local Similarity 51.9%; Pred.No. 0.00097;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 KYSLPFLDYDFSATEPYISGQINEIXY 27
    ||| | | | | | | | | | | | | |
Db 9 KYELPPLPNYLDALPEVYSKEIIDVHY 35

RESULT 25
SODM BOVIN
ID - SODM BOVIN STANDARD; PRT; 222 AA.
AC P41976;
DT DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN NCBI
RN SEQUENCE FROM N.A.
RP RP
RC TISSUE=Lung;
RX MEDLINE=94121934; PubMed=8292376;
RA Meyrick B., Magnuson M.A.;
RT "Identification and functional characterization of the bovine
RL manganous superoxide dismutase promoter.";
CC Am. J. Respir. Cell Mol. Biol. 10:113-121(1994).
CC -I- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -I- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -I- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -I- SUBUNIT: Homotetramer (By similarity).
CC -I- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -I- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
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EMBL; L22092; AAA30655.1; ALT_INIT.
DR EMBL; L22093; AAA30656.1; -.
DR EMBL; S67818; AAC60522.2; -.
DR EMBL; S67819; AAD14001.1; -.
DR FIR; I51918; I51918.
DR HSP; P04179; IABM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).
FT METAL 98 98 MANGANESE (BY SIMILARITY).
FT METAL 183 183 MANGANESE (BY SIMILARITY).
FT METAL 187 187 MANGANESE (BY SIMILARITY).
FT CONFLICT 8 8 S -> R (IN REF. 1; AAD14001).
FT CONFLICT 90 90 F -> V (IN REF. 1; AAC60522).
SQ SEQUENCE 222 AA; 24638 MW; 806CC3FCB1AY4413 CRC64;

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Query Match 51.0%; Score 74; DB 1; Length 222;
 Best Local Similarity 42.9%; Pred. No. 0.001;
 Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSTATPEYISQINEIXYT 28
 Db 25 KHSPLDLPYDYGALPHINAQIMQLHHS 52

RESULT 26

SODM HUMAN STANDARD; PRT; 222 AA.
 AC P04179; P78434; Q16792; Q9P223;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89076921; PubMed=2462451;
 RA Wispe J.R., Clark J.C., Burhans M.S., Kropp K.E., Korfhagen T.R.,
 RA Whitsett J.A.;
 RT "Synthesis and processing of the precursor for human
 RT mangano-superoxide dismutase.";
 RL Biochim. Biophys. Acta 994:30-36(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88067716; PubMed=3684581;
 RA Beck Y., Oren R., Amit B., Levanon A., Gorecki M., Hartman J.R.;
 RT "Human Mn superoxide dismutase cDNA sequence.";
 RL Nucleic Acids Res. 15:9076-9076(1987).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT VAL-16.
 RX MEDLINE=88289364; PubMed=339391;
 RA Heckl K.;
 RT "Isolation of cDNAs encoding human manganese superoxide dismutase.";
 RL Nucleic Acids Res. 16:6224-6224(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88152250; PubMed=2831093;
 RA Ho Y.-S., Crapo J.D.;
 RT "Isolation and characterization of complementary DNAs encoding human
 RT manganese-containing superoxide dismutase.";
 RL FEBS Lett. 229:256-260(1988).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=91105727; PubMed=1988135;
 RA St Clair D.K., Holland J.C.;
 RT "Complementary DNA encoding human colon cancer manganese superoxide
 RT dismutase and the expression of its gene in human cells.";
 RL Cancer Res. 51:939-943(1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91027939; PubMed=1699607;
 RA Church S.L.;
 RT "Manganese superoxide dismutase: nucleotide and deduced amino acid
 RT sequence of a cDNA encoding a new human transcript.";
 RL Biochim. Biophys. Acta 1087:250-252(1990).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95217333; PubMed=7702755;
 RA Wan X.S., Devalaraja M.N., St Clair D.K.;
 RT "Molecular structure and organization of the human manganese
 RT superoxide dismutase gene.";
 RL DNA Cell Biol. 13:1127-1136(1994).

RN [8]
 RP SEQUENCE OF 25-222.
 RX MEDLINE=85030346; PubMed=6386798;
 RA Barra D., Schinina M.E., Simmaco M., Bannister J.V., Bannister W.H.,
 RA Rotilio G., Bossa F.;
 RT "The primary structure of human liver manganese superoxide
 RT dismutase.";
 RL J. Biol. Chem. 259:12595-12601(1984).
 RN [9]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [10]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyov L.I., Shishkin S.S., Bfimochkin A.S., Kovalyova M.A.,
 RA Eshova B.S., Egorov T.A., Masalyanov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [11]
 RP SEQUENCE OF 25-39.
 RC TISSUE=Breast carcinoma;
 RX MEDLINE=97295304; PubMed=9150946;
 RA Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
 RA Simpson R.J., Dorow D.S.;
 RT "Two-dimensional electrophoretic analysis of human breast carcinoma
 RT proteins: mapping of proteins that bind to the SH3 domain of mixed
 RT lineage kinase MLK2.";
 RL Electrophoresis 18:588-598(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=93008233; PubMed=1394426;
 RA Borgstahl G.E.O., Parge H.E., Hickey M.J., Beyer W.F. Jr.,
 RA Hallewell R.A., Tainer J.A.;
 RT "The structure of human mitochondrial manganese superoxide dismutase
 RT reveals a novel tetrameric interface of two 4-helix bundles.";
 RL Cell 71:107-118(1992).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF VARIANT THR-82.
 RX MEDLINE=96183289; PubMed=8605177;
 RA Borgstahl G.E.O., Parge H.E., Hickey M.J., Johnson M.J.,
 RA Boissinot M., Hallewell R.A., Lepock J.R., Cabelli D.E.,
 RA Tainer J.A.;
 RT "Human mitochondrial manganese superoxide dismutase polymorphic
 RT variant Ile58Thr reduces activity by destabilizing the tetrameric
 RT interface.";
 RL Biochemistry 35:4287-4297(1996).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF VARIANT ASN-167.
 RX MEDLINE=98206888; PubMed=9537988;
 RA Hsieh Y., Guan Y., Tu C., Bratt P.J., Angerhofer A., Lepock J.R.,
 RA Hickey M.J., Tainer J.A., Nick H.S., Silverman D.N.;
 RT "Probing the active site of human manganese superoxide dismutase: the
 RT role of glutamine 143.";
 RL Biochemistry 37:4731-4739(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF VARIANT TYR-58.
 RX MEDLINE=98206887; PubMed=9537987;
 RA Guan Y., Hickey M.J., Borgstahl G.E.O., Hallewell R.A., Lepock J.R.,
 RA O'Connor D., Hsieh Y., Nick H.S., Silverman D.N., Tainer J.A.;
 RT "Crystal structure of Y34F mutant human mitochondrial manganese
 RT superoxide dismutase and the functional role of tyrosine 34.";
 RL Biochemistry 37:4722-4730(1998).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.13 ANGSTROMS) OF MUTANT ALA-167.
 RX MEDLINE=20311275; PubMed=10852710;
 RA Leveque V.J.-P., Stroupe M.E., Lepock J.R., Cabelli D.E., Tainer J.A.,

QY

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FT CONFLICT 138 138 V -> M (IN REF. 1 AND 3).
SQ SEQUENCE 222 AA; 24603 MW; 9AB804C55A8357D9 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.001;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KYSLPELDYFESATEPYISQINEIXYT 28
   |||:||::|||:||::||::||
Db 25 KHSLPOLPDYGALPHINAQIMQLHRS 52

RESULT 28
SODM RAT STANDARD; PRT; 222 AA.
AC P07895;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=88096516; PubMed=3697077;
RA Ho Y.-S.; Crapo J.D.;
RT "Nucleotide sequences"; of cDNAs coding for rat manganese-containing
RT superoxide dismutase.";
RL Nucleic Acids Res. 15:10070-10070(1987).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=91159005; PubMed=2001291;
RA Ho Y.-S.; Howard A.J.; Crapo J.D.;
RT "Molecular structure of a functional rat gene for manganese-containing
RT superoxide dismutase.";
RL Am. J. Respir. Cell Mol. Biol. 4:278-286(1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
-----
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or send an email to license@isb-sib.ch).
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DR EMBL; Y00497; CAA68549.1; -.
DR EMBL; X56600; CAA39937.1; -.
DR FIR; S21661; DSRIN.
DR HSSP; P041179; IAGW.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MW; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 24 MITOCHONDRION.
FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).

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FT METAL 98 98 MANGANESE (BY SIMILARITY)
FT METAL 183 183 MANGANESE (BY SIMILARITY)
FT METAL 187 187 MANGANESE (BY SIMILARITY)
FT CONFLICT 167 167 Q -> H (IN REF. 1)
SQ SEQUENCE 222 AA; 24674 MW; 8CCCE05857B3138 CRC64;

Query Match 51.0%; Score 74; DB 1; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.001;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISQINEIXY 28
DB 25 KHSLEPDLFYDYGALPHINAQIMQLRHS 52

RESULT 29
SODF_SULSO STANDARD; PRT; 210 AA.
AC P80857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1).
GN SOD OR SSO0316.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX MEDLINE=99098843; PubMed=9880816;
RA Yamano S., Maruyama T.;
RT "An azide-insensitive superoxide dismutase from a hyperthermophilic
archaeon, Sulfolobus solfataricus."
RL J. Biochem. 125:186-193(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RX MEDLINE=21145482; PubMed=11248699;
RA De Vendittis E., Ursby T., Rullo R., Gogliettino M.A., Masullo M.,
RA Bocchini V.;
RT "Phenylmethanesulfonyl fluoride inactivates an archaeal superoxide
dismutase by chemical modification of a specific tyrosine residue:
cloning, sequencing and expression of the gene coding for Sulfolobus
solfataricus superoxide dismutase."
RL Eur. J. Biochem. 268:1794-1801(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiler C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=99134398; PubMed=9931259;
RA Ursby T., Adinolfi B.S., Al-Karadaghi S., de Vendittis E.,
RA Bocchini V.;

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RT "Iron superoxide dismutase from the archaeon Sulfolobus solfataricus:
analysis of structure and thermostability."
RL J. Mol. Biol. 286:189-205(1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC
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CC
CC EMBL; AB012620; BAA75509.1; -.
CC EMBL; Y15326; CAA75583.1; -.
CC EMBL; AE006666; AAK40652.1; -.
CC PIR; E90174; E90174.
CC PDB; 1SSS; 09-APR-99.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sode; 1.
CC DR PRINTS; PR01703; MNSODISMUTASE.
CC DR PRODOM; PD000475; SODismutase; 1.
CC DR PROSITE; PS00088; SOD_MN; FALSE NEG.
CC Oxidoreductase; Metal-binding; Iron; 3D-structure; Complete proteome.
FT INIT_MET 0 0
FT METAL 37 37 IRON.
FT METAL 84 84 IRON.
FT METAL 170 170 IRON.
FT METAL 174 174 IRON.
FT TURN 18 24
FT HELIX 27 35
FT TURN 36 36
FT TURN 37 57
FT TURN 58 58
FT TURN 62 63
FT TURN 67 89
FT TURN 90 90
FT STRAND 91 91
FT STRAND 94 94
FT TURN 95 96
FT STRAND 97 97
FT HELIX 103 113
FT HELIX 116 129
FT STRAND 134 140
FT TURN 142 144
FT STRAND 147 153
FT TURN 154 156
FT STRAND 157 157
FT STRAND 165 170
FT HELIX 173 175
FT TURN 176 176
FT HELIX 177 180
FT TURN 181 182
FT HELIX 184 191
FT HELIX 192 194
FT STRAND 195 195
FT HELIX 197 206
FT TURN 207 207
SQ SEQUENCE 210 AA; 24112 MW; 7918CF1292BF98B6 CRC64;

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Query Match 50.3%; Score 73; DB 1; Length 210;
Best Local Similarity 51.9%; Pred. No. 0.0014;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISQINEIXY 27


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GN SODA OR SODM OR CPN0057 OR CP0718 OR CPB0058.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RT Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RL "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RN Nat. Genet. 21:385-389(1999).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S.,
RT White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RL Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RT Eisen J., Fraser C.M.;
RL "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RN Nucleic Acids Res. 28:1397-1406(2000).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RT Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RL "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RN Nucleic Acids Res. 28:2311-2314(2000).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=TW-183;
RX Geng M.M., Schuchmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RL other Chlamydia strains based on whole genome sequence analysis.";
CC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -|- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -|- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; AE001591; AAD18210.1; -
CC EMBL; AE002230; AAF38524.1; -
CC EMBL; AP002545; BAA98268.1; -
CC EMBL; AE017157; AAP97991.1; -
CC PIR; B72124; B72124.
CC PIR; B86498; B86498.
CC HSSP; P04179; IAF6
CC PHCI-2DPAGE; Q9Z9C4; -.
CC TIGR; CP0718; -.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC Pfam; PF02777; sodfe C; 1.
CC PRINTS; PR01703; MNSODISMUTASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
CC Oxidoreductase; Metal-binding; Iron; Complete proteome.
CC METAL 26 26 IRON (BY SIMILARITY).
CC FT METAL 81 81 IRON (BY SIMILARITY).
CC FT METAL 164 164 IRON (BY SIMILARITY).
CC FT METAL 168 168 IRON (BY SIMILARITY).
CC SEQUENCE 203 AA; 23523 MW; AEA3A24EAC591716 CRC64;
Query Match 48.3%; Score 70; DB 1; Length 203;
Best Local Similarity 44.4%; Pred. No. 0.0037;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
Qy 2 YSPELDYERSATPYISGQINEIXYT 28
:|||||:::|||||:|||||:
Db 2 FKLPGLGYDYDAVEFYIDAKTMELHHS 28
:|||||:::|||||:|||||:
RESULT 35
SODM_CHLPN
ID _SODM_CHLPN STANDARD; PRT; 207 AA.
AC Q9Z9C4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1).

```

DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).

GN SODA.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Leaf;
RC MEDLINE=92032795; PubMed=1932701;
RX Wong-Vega L., Burke J.J., Allen R.D.;
RA "Isolation and sequence analysis of a cDNA that encodes pea manganese
RT superoxide dismutase.";
RL Plant Mol. Biol. 17:1271-1274 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=68;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pressecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche E., Rose M., Sadale I.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker I.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.

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EMBL; X60170; CAA42737.1; -;
EMBL; U30841; AAA74442.1; -;
PIR; S18343; DSPMN.
HSP; P04179; IABM.
InterPro; IPR001189; SODismutase.
Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR PRODOM; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 36 MITOCHONDRION (PROBABLE).
FT CHAIN 37 233 SUPEROXIDE DISMUTASE [MN].
FT METAL 64 64 MANGANESE (BY SIMILARITY).
FT METAL 112 112 MANGANESE (BY SIMILARITY).
FT METAL 194 194 MANGANESE (BY SIMILARITY).
FT METAL 198 198 MANGANESE (BY SIMILARITY).
FT CONFLICT 160 160 Q -> QASGW (IN REF. 1).
FT CONFLICT 176 176 T -> TAN (IN REF. 1).
FT CONFLICT 192 192 G -> W (IN REF. 1).
SQ SEQUENCE 233 AA; 25822 MW; DB246D1FF0AF4FF9 CRC64;
Query Match 48.3%; Score 70; DB 1; Length 233;
Best Local Similarity 46.2%; Pred. No. 0.0042;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 YSLPELYEFSATPEYISGQNEIXY 27
Db 40 FTLPDLAYDYGALEPVISGEIMQIH 65

RESULT 38
SODF_BACSU
ID -SODF_BACSU STANDARD; PRT; 281 AA.
AC O35023;
DT 30-MAY-2000 (Rel. 39, Created)

Qy 4 LPELDYEFSATEPYISGQINEIXY 27
||| : ||| : ||| :
Db 5 LPDLPAYDALEPYISRQIMELHH 28

Search completed: August 24, 2004, 23:01:02
Job time : 24 secs

C;Accession: S06599; A37212
R;hangaraj, H.S.; Lamb, F.I.; Davis, E.O.; Colston, M.J.
Nucleic Acids Res. 17, 8378, 1989

A;Title: Nucleotide and deduced amino acid sequence of Mycobacterium leprae manganese su-
A;Reference number: S06599; MUID:90045970; PMID:2682526

A;Accession: S06599
A;Molecule type: DNA
A;Residues: 1-207 <THA>
A;Cross-references: EMBL:X16453; NID:g44405; PIDN.CAA34472.1; PID:g581343
R;hangaraj, H.S.; Lamb, F.I.; Davis, E.O.; Jenner, P.J.; Jeyakumar, L.H.; Colston, M.J.
Infect. Immun. 58, 1937-1942, 1990

A;Title: Identification, sequencing, and expression of Mycobacterium leprae superoxide d-
A;Reference number: A37212; MUID:90256282; PMID:1692812

A;Accession: A37212
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'V', 2-207 <TH2>
A;Cross-references: GB:X16453

C;Genetics:
C;Start codon: GTG

C;Function:
A;description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase
F;28,76,160,164/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 67.6%; Score 98; DB 2; Length 207;
Best Local Similarity 57.1%; Pred. No. 2,9e-07;
Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KYSLPELDVFSTATPYISQGINEIYYT 28
Db 3 EYLPDLWDYAALPEHPSGEINIIHT 30

RESULT 5

S15205
superoxide dismutase (EC 1.15.1.1) [Fe] [validated] - Mycobacterium tuberculosis
C/Species: Mycobacterium tuberculosis
C/Date: 21-Nov-1993 #sequence revision 26-May-1995 #text_change 20-Jun-2000
C/Accession: S15205; C70654; S10908
R/Zhang, Y.; Lathigra, R.; Garbe, T.; Catty, D.; Young, D.
Mol. Microbiol. 5, 381-391, 1991
A/Title: Genetic analysis of superoxide dismutase, the 23 kilodalton antigen of Mycobacterium tuberculosis
A/Reference number: S15205; MUID:91251768; PMID:1904126
A/Accession: S15205
A/Molecule type: DNA
A/Residues: 1-207 <2HA>
A/Cross-references: EMBL:X52861; NID:g794079; PIDN:CAA37042.1; PID:g581379
A/Experimental source: strain H37Rv
A/Note: the authors translated the codon GAA for residue 3 as Gln
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hollroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Young, D.; Parkhill, J.; Whitehead, S.; Barrell, B.G.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: C70654
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-207 <COL>
A/Cross-references: GB:Z83864; GB:AL123456; NID:g3261687; PIDN:CAB06220.1; PID:gl781110
A/Experimental source: strain H37Rv
R/Cooper, J.B.; McIntyre, K.; Wood, S.P.; Zhang, Y.; Young, D.
Submitted to the Brookhaven Protein Data Bank, September 1994
A/Reference number: A52807; PDB:1IDS
A/Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 2-199
R/Cooper, J.B.; Driessen, H.P.C.; Wood, S.P.; Zhang, Y.; Young, D.
J. Mol. Biol. 235, 1156-1158, 1994
A/Title: Crystallisation and preliminary X-ray analysis of the iron-dependent superoxide dismutase from Mycobacterium tuberculosis
A/Reference number: A59029; MUID:94118350; PMID:8289318
A/Contents: annotation; X-ray crystallography

C:Genetics:
A:Gene: soda
A:Start codon: GTG
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: iron; metalloprotein; oxidoreductase; tetramer
F:2,28,76,160,164/Binding site: iron (His, His, Asp, His) #status experimental

Query Match 64.8%; Score 94; DB 2; Length 207;
Best Local Similarity 53.6%; Pred. No. 1.2e-06;
Matches 15; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAATEPYISQINEIXYT 28
DB 3 EYLPDLWDYGALEPHISQINELHHS 30

RESULT 6
JC4396
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) [validated] - Propionibacterium freudenreichii
C:Species: Propionibacterium freudenreichii subsp. shermanii
C:Date: 20-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 20-Apr-2000
C:Accession: JC4396; S41106
R:Gabbianelli, R.; Battistoni, A.; Polizio, F.; Carri, M.T.; De Martino, A.; Meier, B.; Biochem. Biophys. Res. Commun. 216, 841-847, 1995
A:Title: Metal uptake of recombinant cambialistic superoxide dismutase from Propionibacterium freudenreichii
A:Reference number: JC4396; MUID:96074560; PMID:7488202
A:Accession: JC4396
A:Molecule type: DNA
A:Residues: 1-202 <GAB>
A:Cross-references: EMBL:X91650
A:Experimental source: PZ3
R:Meier, B.; Seim, A.P.; Schinina, M.E.; Barra, D. Eur. J. Biochem. 219, 463-468, 1994
A:Title: In vivo incorporation of copper into the iron-exchangeable and manganese-exchangeable sites.

A:Reference number: S41106; MUID:94139724; PMID:8307013
A:Accession: S41106
A:Molecule type: protein
A:Residues: 2-202 <MEI>
A:Experimental source: strain PZ3

C:Genetics:
A:Gene: sod
C:Complex: homotetramer
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
A:Note: can use iron or manganese as cofactor
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: homotetramer; iron; manganese; metalloprotein; oxidoreductase
F:2-202/Product: superoxide dismutase #status experimental <MAT>
F:2,28,76,162,166/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 62.8%; Score 91; DB 2; Length 202;
Best Local Similarity 61.5%; Pred. No. 3.2e-06;
Matches 16; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATEPYISQINEIXY 27
DB 4 YTLPELPDYSALEPYISQINEIMELHH 29

RESULT 7
A38461
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Methylobacterium sp.
C:Species: Methylobacterium sp.
C:Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 20-Apr-2000
C:Accession: A38461; A61532; B61532
R:Matsumoto, T.; Terauchi, K.; Isobe, T.; Matsuo, K.; Yamakura, F. Biochemistry 30, 3210-3216, 1991
A:Title: Iron- and manganese-containing superoxide dismutases from Methylobacterium sp.
A:Reference number: A38461; MUID:91182736; PMID:1848999
A:Accession: A38461

A:Molecule type: protein
A:Residues: 1-202 <MAT>
R:Yamakura, F.; Matsumoto, T.; Terauchi, K. Free Radic. Res. Commun. 12, 329-334, 1991
A:Title: Isolation of Mn-SOD and low active Fe-SOD from Methylobacterium sp.
A:Reference number: A61532
A:Accession: A61532
A:Molecule type: protein
A:Residues: 1-32 <YAM>
A:Note: identical sequences were determined for Fe-SOD and Mn-SOD; these were shown in r
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: iron; manganese; metalloprotein; oxidoreductase
F:26,80,163,167/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 52.4%; Score 76; DB 2; Length 202;
Best Local Similarity 51.9%; Pred. No. 0.0006;
Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 YSLPELDYFSAATEPYISQINEIXYT 28
DB 2 YTLPELPDYATALEPHIDAQTMEIHHT 28

RESULT 8
DSHUN
superoxide dismutase (EC 1.15.1.1) (Mn) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 06-Feb-1995 #text_change 20-Apr-2000
C:Accession: S13162; S02272; S11756; S00356; S02230; S00663; A92447; I38033; A00520; A27
R:Church, S.L. Biochim. Biophys. Acta 1087, 250-252, 1990
A:Title: Manganese superoxide dismutase: nucleotide and deduced amino acid sequence of a
A:Reference number: S13162; MUID:91027939; PMID:1699607
A:Accession: S13162
A:Molecule type: mRNA
A:Residues: 1-222 <CHU>
A:Note: cross-reference GB:M34665 cited in paper is not correct
R:Wise, J.R.; Clark, J.C.; Burhans, M.S.; Kropp, K.E.; Korfhagen, T.R.; Whitsett, J.A. Biochim. Biophys. Acta 994, 30-36, 1989
A:Title: Synthesis and processing of the precursor for human manganese-superoxide dismutase
A:Reference number: S02272; MUID:89076921; PMID:2462451
A:Accession: S02272
A:Molecule type: mRNA
A:Residues: 1-81, 'T', 83-222 <WIS>
A:Cross-references: EMBL:X14322; NID:G34706; PIDN:CAA32502.1; PID:G34707
R:StClair, D.K.
submitted to the EMBL Data Library, April 1989
A:Description: Nucleotide sequence of a human tumor MnSOD cDNA.
A:Reference number: S11756
A:Accession: S11756
A:Molecule type: mRNA
A:Residues: 1-64, 'N', 66-222 <EMB>
A:Cross-references: EMBL:X15132; NID:G34794; PIDN:CAA33228.1; PID:G34795
R:Ho, Y.S.; Crapo, J.D. PERS Lett. 229, 256-260, 1988
A:Title: Isolation and characterization of complementary DNAs encoding human manganese-c
A:Reference number: S00356; MUID:88152250; PMID:2831093
A:Accession: S00356
A:Molecule type: mRNA
A:Residues: 1-81, 'T', 83-222 <HO1>
A:Cross-references: EMBL:Y00985; NID:G36536; PIDN:CAA68791.1; PID:G36537
R:Heckl, K.
Nucleic Acids Res. 16, 6224, 1988
A:Title: Isolation of cDNAs encoding human manganese superoxide dismutase.
A:Reference number: S02230; MUID:88289364; PMID:3399391
A:Accession: S02230
A:Molecule type: mRNA
A:Residues: 1-13, 'P', 15, 'Y', 17-122, 'L', 124-222 <HEC>
A:Cross-references: EMBL:X07834; NID:G36517; PIDN:CAA30687.1; PID:G36518
A:Note: the authors translated the codon CTG for residue 123 as Arg
R:Beck, Y.; Oren, R.; Amit, B.; Levanon, A.; Gorecki, M.; Hartman, J.R.

Nucleic Acids Res. 15, 9076, 1987

A;Title: Human Mn superoxide dismutase cDNA sequence.
A;Reference number: S00563; MUID:88067716; PMID:3694581
A;Accession: S00563

A;Molecule type: mRNA

A;Residues: 1-154,'Q',156-222 <BEC>

A;Cross-references: EMBL:Y00472; NID:g34710; PIDN:CAA68533.1; PID:g34711
R;Barra, D.; Schinina, M.E.; Simmaco, M.; Bannister, J.V.; Rotilio, G.;
J. Biol. Chem. 259, 12595-12601, 1984

A;Title: The primary structure of human liver manganese superoxide dismutase.

A;Reference number: A92447; MUID:85030346; PMID:6396798

A;Accession: A92447

A;Molecule type: protein

A;Residues: 25-65,'O',67-111,'Q',113-132,'Q',134-147,150-154,'Q',156-222 <BAR>

R;St Clair, D.K.; Holland, J.C.

Cancer Res. 51, 939-943, 1991

A;Title: Complementary DNA encoding human colon cancer manganese superoxide dismutase and

A;Reference number: I38033; MUID:91105727; PMID:1988135

A;Accession: I38033

A;Status: Preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-64,'N',66-222 <RES>

A;Cross-references: EMBL:X59472; NID:g34708; PIDN:CAA42066.1; PID:g34709

R;Borgstahl, G.E.O.; Parge, H.E.; Hickey, M.J.; Beyer Jr., W.F.; Hallewell, R.A.; Tainer
Cell 71, 107-118, 1992

A;Title: The structure of human mitochondrial manganese superoxide dismutase reveals a n

A;Reference number: A43483; MUID:93008233; PMID:1394426

A;Contents: annotation; X-ray crystallography, 2.2 angstroms

R;Borgstahl, G.E.O.; Parge, H.E.; Tainer, J.A.

submitted to the Brookhaven Protein Data Bank, August 1992

A;Reference number: A51016; PDB:IABM

A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 25-222

A;Note: Kidney recombinant form expressed in *Escherichia coli*

R;Sussman, J.; Wagner, U.G.; Pattidge, K.A.; Ludwig, M.L.

submitted to the Brookhaven Protein Data Bank, November 1992

A;Reference number: A51304; PDB:IMSD

A;Contents: annotation; X-ray crystallography, 3.2 angstroms, residues 25-222

C;Genetics:

A;Gene: GDB:SOD2

A;Cross-references: GDB:119597; OMIM:147460

A;Map position: 6q25.2-6q25.2

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase

F;1-24/Domain: transit peptide (mitochondrion) #status predicted <INP>

F;25-222/Product: superoxide dismutase (Mn) #status experimental <MAT>

F;50,98,183,187/Binding site: manganese (His, Asp, His) #status experimental

Query Match

Best Local Similarity 51.0%; Score 74; DB 1; Length 222;

Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAPEYISGQINEIXYT 28

Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 9

DSSTN

superoxide dismutase (EC 1.15.1.1) (Mn) precursor - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999

C;Accession: S21661; S06310

R;Ho, Y.S.; Howard, A.G.; Crapo, J.D.

submitted to the EMBL Data Library, October 1990

A;Reference number: S21661

A;Accession: S21661

A;Molecule type: DNA

A;Residues: 1-222 <HOY1>

A;Cross-references: EMBL:X56600; NID:g57272; PIDN:CAA39937.1; PID:g57273

R;Ho, Y.S.; Crapo, J.D.

Nucleic Acids Res. 15, 10070, 1987

A;Title: Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide

A;Reference number: S06310; MUID:88096516; PMID:3697077

A;Accession: S06310

A;Molecule type: mRNA

A;Residues: 1-166,'H',168-222 <HOY2>

A;Cross-references: EMBL:Y00497; NID:g56690; PIDN:CAA68549.1; PID:g56691

A;Note: 167-Gln was also found

C;Genetics:

A;Gene: SOD2

A;Introns: 8/2; 76/1; 115/1; 175/1

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase

F;1-24/Domain: transit peptide (mitochondrion) #status predicted <INP>

F;25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>

F;50,98,183,187/Binding site: manganese (His, Asp, His) #status predicted

Query Match

Best Local Similarity 51.0%; Score 74; DB 1; Length 222;

Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYFSAPEYISGQINEIXYT 28

Db 25 KHSPLDLPDYGALEPHINAQIMQLHHS 52

RESULT 10

I57023

superoxide dismutase (EC 1.15.1.1) (Mn) precursor - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Jun-1999

C;Accession: I57023; JC4047; S36129; A25581

R;DiSilvestre, D.; Kleeberger, S.R.; Johns, J.; Levitt, R.C.

Mamm. Genome 6, 281-284, 1995

A;Title: Structure and DNA sequence of the mouse MnSOD gene.

A;Reference number: I57023; MUID:95337589; PMID:7613035

A;Accession: I57023

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-222 <RES>

A;Cross-references: GB:S78846; NID:g1037119; PIDN:AAB34899.1; PID:g1037120

R;Jones, P.L.; Kucera, G.; Gordon, H.; Boss, J.M.

Gene 153, 155-161, 1995

A;Title: Cloning and characterization of the murine manganese superoxide dismutase-encod

A;Reference number: JC4047; MUID:95180711; PMID:7875582

A;Accession: JC4047

A;Molecule type: DNA

A;Residues: 1-137,'M',139-222 <JON>

A;Cross-references: GB:I35525

R;Sun, Y.

submitted to the EMBL Data Library, November 1992

A;Reference number: S36129

A;Accession: S36129

A;Molecule type: mRNA

A;Residues: 1-222 <JON>

A;Cross-references: EMBL:Z18857; NID:g288504; PIDN:CAA79308.1; PID:g288505

R;Hallewell, R.A.; Mullenbach, G.T.; Stempien, M.M.; Bell, G.I.

Nucleic Acids Res. 14, 9539, 1986

A;Title: Sequence of a cDNA coding for mouse manganese superoxide dismutase.

A;Reference number: A25581; MUID:87091590; PMID:3797253

A;Accession: A25581

A;Molecule type: mRNA

A;Residues: 1-17,'V',19-137,'M',139-222 <HAL>

A;Cross-references: GB:X04972; NID:g53449; PIDN:CAA28645.1; PID:g53450

C;Genetics:

A;Gene: Sod-2

A;Introns: 8/2; 76/1; 115/1; 175/1

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase

F;1-24/Domain: transit peptide (mitochondrion) #status predicted <INP>

F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0014;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXYT 28
DB 25 KHSPLDPLPYDYGALPEFHNAQIMQLHHS 52

RESULT 11

151918
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence revision 15-Aug-1997 #text_change 21-Jul-2000
C:Accession: I51918; I64848; I64850
R:Meyrick, B.; Magnuson, M.A.
A>Title: Identification and functional characterization of the bovine manganous superoxide dismutase
A:Reference number: I51918; MUID:94121934; PMID:8292376
A:Accession: I51918
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-222 <MEY1>
A:Cross-references: GB:L22092; NID:g498259; PIDN:AAA30655.1; PID:g498260
A:Accession: I64848
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-7 <MEY2>
A:Cross-references: GB:L22093; NID:g498261; PIDN:AAA30656.1; PID:g552330
A:Accession: I64850
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-7, 'R' <MEY3>
A:Cross-references: GB:S67819; NID:g460572; PIDN:AAD14001.1; PID:g4261701
C:Genetics:
A:Gene: MnSOD
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.0%; Score 74; DB 2; Length 222;
Best Local Similarity 42.9%; Pred. No. 0.0014;
Matches 12; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXYT 28
DB 25 KHSPLDPLPYDYGALPEFHNAQIMQLHHS 52

RESULT 12
T08181
superoxide dismutase (EC 1.15.1.1) (Mn) - radish
C:Species: Raphanus sativus (radish)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Apr-2000
C:Accession: T08181
R:Kwon, S.I.; An, C.S.
A:Reference number: Z16401
A:Accession: T08181
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-231 <KWO>
A:Cross-references: EMBL:AF061333; NID:g3108344; PID:g3108345
C:Genetics:
A:Gene: sod
C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; oxidoreductase
F:51,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 51.0%; Score 74; DB 2; Length 231;
Best Local Similarity 50.0%; Pred. No. 0.0014;
Matches 13; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEYISGQINEIXY 27
DB 31 FTLPLDPLPYDYGALPEFAISGEIMQIH 56

RESULT 13

E90174
superoxide dismutase [Fe] (sod) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: E90174
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: E90174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KUR>
A:Cross-references: GB:AB006641; NID:gi3813460; PIDN:AAK40652.1; GSPDB:GN00155
C:Genetics:
A:Gene: sod
C:Superfamily: superoxide dismutase (Mn)

Query Match 50.3%; Score 73; DB 2; Length 211;
Best Local Similarity 51.9%; Pred. No. 0.0018;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 KYSLPELDYEFSAPEYISGQINEIXY 27
DB 9 KYELPPLPYKIDALEFYISKDIDVHY 35

RESULT 14

T08045
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - pepper
C:Species: Capsicum annuum (pepper)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 20-Apr-2000
C:Accession: T08045
R:Li, K.S.; Sun, A.C.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z16312
A:Accession: T08045
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-228 <ILK>
A:Cross-references: EMBL:AF036936; NID:g2687664; PIDN:AA88870.1; PID:g2687665
C:Genetics:
A:Gene: SOD
A:Genome: nuclear
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:52,100,189,193/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.7%; Score 72; DB 2; Length 228;
Best Local Similarity 46.2%; Pred. No. 0.0028;
Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEYISGQINEIXY 27

Db 28 FSLPDLSDYDGALEPAISGEIMQLHH 53

RESULT 15

T50829

superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Para rubber tree (fragment)

C:Species: Hevea brasiliensis (Para rubber tree)

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000

C:Accession: T50829

R:Wagner, S.; Breiteneder, H.

submitted to the EMBL Data Library, August 1999

A:Description: Cloning and molecular characterization of MnSOD; a cross-reactive allergen

A:Reference number: Z25248

A:Accession: T50829

A:Status: preliminary; translated from GB/EMBL/DBU

A:Molecule type: mRNA

A:Residues: 1-205 <WAG>

A:Cross-references: EMBL:AJ249148; PIDN:CA53458.1

C:Genetics:

A:Gene: sod

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; oxidoreductase

F:27,75,164,168/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.0%; Score 71; DB 2; Length 205;

Best Local Similarity 46.2%; Pred. No. 0.0035; 6; Indels 0; Gaps 0;

Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIXY 27

Db 3 FSLPDLSDYDGALEPAISGEIMQLHH 28

RESULT 16

S39492

superoxide dismutase (EC 1.15.1.1) (Mn) - Para rubber tree

C:Species: Hevea brasiliensis (Para rubber tree)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999

C:Accession: S39492

R:Miao, Z.; Gaynor, J.J.

A:Title: Molecular cloning, characterization and expression of Mn-superoxide dismutase

A:Reference number: S39492; MUID:94033306; PMID:8219064

A:Accession: S39492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <MIA>

A:Cross-references: GB:L11707; NID:g348136; PIDN:AAAL6792.1; PID:g348137

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; oxidoreductase

F:55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.0%; Score 71; DB 2; Length 233;

Best Local Similarity 46.2%; Pred. No. 0.0041;

Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIXY 27

Db 31 FSLPDLSDYDGALEPAISGEIMQLHH 56

RESULT 17

T50830

superoxide dismutase (EC 1.15.1.1) (Mn) precursor, mitochondrial [similarity] - leafy sp

C:Species: Euphorbia esula (leafy spurge)

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000

C:Accession: T50830

R:Anderson, J.V.; Horvath, D.P.

submitted to the EMBL Data Library, March 2000

A:Description: Identification of mRNAs expressed in underground adventitious buds of Eup

A:Reference number: Z25249

A:Accession: T50830

A:Status: preliminary; translated from GB/EMBL/DBU

A:Molecule type: mRNA

A:Residues: 1-237 <AND>

A:Cross-references: EMBL:AF242310; PIDN:AAF65768.1

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; mitochondrial; oxidoreductase

F:60,108,196,200/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.0%; Score 71; DB 2; Length 237;

Best Local Similarity 46.2%; Pred. No. 0.0042;

Matches 12; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQINEIXY 27

Db 36 FSLPDLSDYDGALEPAISGEIMQLHH 61

RESULT 18

B86498

superoxide dismutase (Mn) [imported] - Chlamydomonas pneumoniae (strain J138)

C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: B86498

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: B86498

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-207 <STO>

A:Cross-references: GB:BA000008; NID:g978431; PIDN:BA98268.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: sodM

C:Superfamily: superoxide dismutase (Mn)

Query Match 48.3%; Score 70; DB 2; Length 207;

Best Local Similarity 61.9%; Pred. No. 0.005;

Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSSATEPYISQI 22

Db 6 YSLPELDYDGALEPAISSEI 26

RESULT 19

B72124

superoxide dismutase (EC 1.15.1.1) (Mn) CP0718 [similarity] - Chlamydomonas pneumoniae

C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000

C:Accession: B72124; B81547

R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: B72124

A:Molecule type: DNA

A:Residues: 1-207 <ARN>

A:Cross-references: GB:AE001591; GB:AE001363; NID:g4376311; PIDN:AA018210.1; PID:g437631

A:Experimental source: strain CWL029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, P.

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: AB1500; MUID:20150255; PMID:10684935

A:Accession: B81547

A:Molecule type: DNA

A:Residues: 1-207 <REA>

A:Cross-references: GB:AB002230; GB:AB002161; NID:g7189624; PIDN:AAF38524.1; PID:g718963

A:Experimental source: strain AR39, HL cells

C:Genetics:

A;Gene: sodM; CP0718
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;30,78,166,170/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 48.3%; Score 70; DB 2; Length 207;
Best Local Similarity 61.9%; Pred. No. 0.005; Gaps 0;
Matches 13; Conservative 3; Mismatches 5; Indels 0;

Qy 2 YSLPELDYEFSAATEPYISGQI 22
||||| : : | : :
Db 6 YSLPELPDYDDALEPVISEI 26
||||| : : | : :
||| : : | : :

RESULT 20
A70119
Superoxide dismutase [EC 1.15.1.1] (Fe/Mn) soda homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-May-2000
C;Accession: A70119
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; PMID:98065943; PMID:9403685
A;Accession: A70119
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-214 <KLE>
A;Cross-references: GB:AE000126; GB:AE000783; NID:g2688035; PIDN:AAC66537.1; PID:g2688035
A;Experimental source: strain B31
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: iron; manganese; metalloprotein; oxidoreductase
F;37,92,175,179/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 48.3%; Score 70; DB 2; Length 214;
Best Local Similarity 44.4%; Pred. No. 0.0052; Gaps 0;
Matches 12; Conservative 6; Mismatches 9; Indels 0;

Qy 2 YSLPELDYEFSAATEPYISGQINEIXYT 28
:||| ||| : : : : :
Db 13 FKPLGLGYDVAEPVIDAKTMEIHHS 39
:||| ||| : : : : :
||| : : | : : :

RESULT 21
TS0827
Superoxide dismutase [EC 1.15.1.1] (Mn) [similarity] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 24-Oct-2000
C;Accession: T50827
R;Kliebenstein, D.J.; Monde, R.A.; Last, R.L.
Plant Physiol. 118, 637-650, 1998
A;Title: Superoxide dismutase in Arabidopsis: an eclectic enzyme family with disparate r
A;Reference number: Z25246; MUID:38440686; PMID:9765550
A;Accession: T50827
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-231 <KLII>
A;Cross-references: EMBL:AF061518; PIDN:AAC24832.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: MSD1
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 48.3%; Score 70; DB 2; Length 231;
Best Local Similarity 46.2%; Pred. No. 0.0058; Gaps 0;
Matches 12; Conservative 8; Mismatches 6; Indels 0;

Query Match 48.3%; Score 70; DB 2; Length 281;
Best Local Similarity 50.0%; Pred. No. 0.0073;
Matches 14; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 KYSLPELDYVSATPYISGOINEIXYT 28
DB 79 KHVLPKLPYKYSALEPYSIRDMILHHT 106

||||| :||| ||||| | :|
| :||| :||| ||||| | :|

RESULT 24

S03639
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - curled-leaved tobacco
C:Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 07-Dec-1999
C:Accession: S03639
R:Bowler, C.; Alliotte, T.; de Loose, M.; van Montagu, M.; Inze, D.
EMBO J. 8, 31-38, 1989
A>Title: The induction of manganese superoxide dismutase in response to stress in Nicotiana glauca
A:Reference number: S03639; MUID:89231633; PMID:2540959
A:Accession: S03639
A:Molecule type: mRNA
A:Residues: 1-228 <BOW>
A:Cross-references: EMBL:X14482; NID:gl9692; PIDN:CMA32643.1; PID:gl9693
A:Experimental source: cv. P2
C:Genetics:
A:Genome: nuclear
C:Function:
A>Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-228/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:52.100,189,193/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 47.6%; Score 69; DB 2; Length 228;
Best Local Similarity 46.2%; Pred. No. 0.008;
Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYVSATPYISGOINEIXY 27
DB 28 FSLPELDYDYGALPEAISGDIQLHH 53

||||| :||| ||||| | :|
| :||| :||| ||||| | :|

RESULT 25

G82535
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Aug-2001
C:Accession: G82535
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: G82535
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <SIM>
A:Cross-references: GB:AE004068; GB:AE003849; NID:g9107832; PIDN:AAF85411.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abranches, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.; Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.I.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret-Chado, M.A.; Madeira, A.M.B.F.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, W.A.; da Silva Jr., W.A.; da Silveira, M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zingales, R.; Reference number: A59328

A;Contents: annotation
C;Genetics:
A;Gene: XP2614
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: metalloprotein; oxidoreductase

Query Match 46.9%; Score 68; DB 2; Length 203;
Best Local Similarity 48.1%; Pred. No. 0.0099;
Matches 13; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

DQ 2 YSLPELDYFESATEPYISGQINEIXYT 28
| : | | | : | : | : | : | : | : |
DB 3 YTLPLPYAYDALQPHIDAQTMEIHYT 29

RESULT 26

S65795
superoxide dismutase (EC 1.15.1.1) (Mn) - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Mar-1999
C;Accession: S65795
R;Yuan, H.T.; Bingle, C.D.; Kelly, F.J.
Biochim. Biophys. Acta 1305, 163-171, 1996
A;Title: Differential patterns of antioxidant enzyme mRNA expression in guinea pig lung
A;Reference number: S65793; MUID:96180320; PMID:8597602
A;Accession: S65795
A;Molecule type: mRNA
A;Residues: 1-204 <YUA>
A;Cross-references: EMBL:U39843
C;Genetics:
A;Genome: nuclear
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;43,91,176,180/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 204;
Best Local Similarity 35.7%; Pred. No. 0.0099;
Matches 10; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DQ 1 KYSLPELDYFESATEPYISGQINEIXYT 28
| : | | | : | : | : | : | : | : |
DB 18 KHSLPDLPDYDALQPHINAEIMQLHHS 45

RESULT 27

S34616
superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Sulfolobus acidocaldarius
C;Species: Sulfolobus acidocaldarius
C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S34616
R;Klenk, H.P.; Schleper, C.; Schwass, V.; Brudler, R.
Biochim. Biophys. Acta 1174, 95-98, 1993
A;Title: Nucleotide sequence, transcription and phylogeny of the gene encoding the superoxide dismutase from Sulfolobus acidocaldarius
A;Reference number: S34615; MUID:93326644; PMID:8334170
A;Accession: S34616
A;Molecule type: DNA
A;Residues: 1-211 <KLE>
A;Cross-references: EMBL:X63386; NID:g396201; PID:g396203
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: iron; manganese; metalloprotein; oxidoreductase
F;34,85,171,175/Binding site: iron/manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 0.01;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

DQ 1 KYSLPELDYFESATEPYISGQINEIXY 27
| : | | | : | : | : | : | : | : |
DB 9 RYEFPOLPYKVDALEPIYSKDIIIVHY 35

RESULT 28

T42080
 superoxide dismutase (EC 1.15.1.1) (Fe-Zn) sodF [validated] - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Oct-2000
 C:Accession: T42080; S74129
 R:Kim, E.J.; Chung, H.J.; Suh, B.; Hah, Y.C.; Roe, J.H.
 J. Bacteriol. 180, 2014-2020, 1998
 A:Title: Expression and regulation of the sodF gene encoding iron- and zinc-containing SOD
 A:Reference number: Z22061; MUID:98215165; PMID:9555880
 A:Accession: T42080
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-213 <KIM>
 A:Cross-references: EMBL:AF012087; NID:g2707212; PIDN:AAC46274.1; PID:g2707213
 R:Kim, E.J.; Kim, H.P.; Hah, Y.C.; Roe, J.H.
 Eur. J. Biochem. 241, 178-185, 1996
 A:Title: Differential expression of superoxide dismutases containing Ni and Fe/Zn in Streptomyces coelicolor
 A:Reference number: S74128; MUID:97054607; PMID:8898904
 A:Accession: S74129
 A:Molecule type: protein
 A:Residues: 2-16 <KI2>
 A:Experimental source: ATCC 10147
 C:Genetics:
 A:Gene: sodF
 C:Function:
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C:Superfamily: superoxide dismutase (Mn)
 C:Keywords: iron; metalloprotein; oxidoreductase; tetramer; zinc
 F:2-113/Product: superoxide dismutase (Fe-Zn) #status experimental <MAT>
 F:28,76,165,169/Binding site: iron (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 213;
 Best Local Similarity 50.0%; Pred. No. 0.01;
 Matches 13; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 27

Db 4 YTLPELDYDYSALAPVISPEITELHH 29

RESULT 29

T06801
 Probable superoxide dismutase (EC 1.15.1.1) (Mn) precursor - wheat
 C:Species: Triticum aestivum (common wheat)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 C:Accession: T06801
 R:Wu, G.; Robertson, A.J.; Wilen, R.W.; Gusta, L.V.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z15825
 A:Accession: T06801
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-231 <WUG>
 A:Cross-references: EMBL:U73172; NID:gl654386; PIDN:AAB68036.1; PID:gl654387
 C:Genetics:
 A:Gene: SOD3.2
 C:Function:
 A:Description: catalyzes the dismutation of superoxide radicals
 C:Superfamily: superoxide dismutase (Mn)
 C:Keywords: manganese; metalloprotein; oxidoreductase
 F:55,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 231;
 Best Local Similarity 42.3%; Pred. No. 0.012;
 Matches 11; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYFSATEPYISQINEIXY 27

Db 31 FTLPELDYDYSALAPVISPEITELHH 56

RESULT 30

C48684
 superoxide dismutase (EC 1.15.1.1) (Mn) 3.4 precursor - maize
 C:Species: Zea mays (maize)
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Apr-2000
 C:Accession: C48684
 R:Zhu, D.; Scandalios, J.G.
 Proc. Natl. Acad. Sci. U.S.A. 90, 9310-9314, 1993
 A:Title: Maize mitochondrial manganese superoxide dismutases are encoded by a differentially expressed gene
 A:Reference number: A48684; MUID:94022365; PMID:8415698
 A:Accession: C48684
 A:Molecule type: mRNA
 A:Residues: 1-232 <ZHU>
 A:Cross-references: GB:L19463
 A:Experimental source: line W64A, embryos
 A>Note: the authors translated the codon GCC for residue 48 as Val and AGG for residue 1
 C:Function:
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C:Superfamily: superoxide dismutase (Mn)
 C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
 F:1-29/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F:57,105,193,197/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 232;
 Best Local Similarity 48.0%; Pred. No. 0.012;
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 SLPELDYFSATEPYISQINEIXY 27

Db 34 ALPDLSDYDFGALEPVISGEIMRLHH 58

RESULT 31

A48684
 superoxide dismutase (EC 1.15.1.1) (Mn) 3.3 precursor - maize
 C:Species: Zea mays (maize)
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Apr-2000
 C:Accession: A48684
 R:Zhu, D.; Scandalios, J.G.
 Proc. Natl. Acad. Sci. U.S.A. 90, 9310-9314, 1993
 A:Title: Maize mitochondrial manganese superoxide dismutases are encoded by a differentially expressed gene
 A:Reference number: A48684; MUID:94022365; PMID:8415698
 A:Accession: A48684
 A:Molecule type: mRNA
 A:Residues: 1-233 <ZHU>
 A:Cross-references: GB:L19462
 A:Experimental source: line W64A, embryos
 A>Note: the authors translated the codon ATC for residue 76 as Leu and AGG for residue 1
 C:Function:
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C:Superfamily: superoxide dismutase (Mn)
 C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
 F:1-29/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F:57,105,194,198/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 233;
 Best Local Similarity 48.0%; Pred. No. 0.012;
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 SLPELDYFSATEPYISQINEIXY 27

Db 34 ALPDLSDYDFGALEPVISGEIMRLHH 58

RESULT 32

T50831
 superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Zantedeschia aethiopica
 C:Species: Zantedeschia aethiopica
 C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
 C:Accession: T50831
 R:Lino-Neto, T.; Tavares, R.M.; Palme, K.; Pais, M.S.S.
 submitted to the EMBL Data Library, September 1998

A;Description: Expression of superoxide dismutases during senescence and regreening of Z
 A;Reference number: Z25250
 A;Accession: T50831
 A;Status: preliminary; translated from GB/EMBL/DBSU
 A;Molecule type: mRNA
 A;Residues: 1-240 <LIN>
 A;Cross-references: EMBL:AF094832; PIDN:AAC63379.1
 C;Genetics:
 A;Gene: Mnsod
 C;Superfamily: superoxide dismutase (Mn)
 C;Keywords: manganese; metalloprotein; oxidoreductase
 F:64,112,201,205/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.9%; Score 68; DB 2; Length 240;
 Best Local Similarity 46.2%; Pred. No. 0.012;
 Matches 12; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAATEPYISQINEIXY 27
 DB 40 FSLPDLFYDGSLEPAISGEIMRIHH 65

RESULT 33
 S39871
 superoxide dismutase (EC 1.15.1.1) (Mn) - Haemophilus influenzae (strain Eagan)
 C;Species: Haemophilus influenzae
 A;Variety: strain Eagan
 C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C;Accession: S39871
 R;Kroll, J.S.; Langford, P.R.; Saah, J.R.; Loynds, B.M.
 Mol. Microbiol. 10, 839-848, 1993
 A;Title: Molecular and genetic characterization of superoxide dismutase in Haemophilus i
 A;Reference number: S39871; MUID:95020555; PMID:7934846
 A;Accession: S39871
 A;Molecule type: DNA
 A;Residues: 1-211 <KRO>
 A;Cross-references: EMBL:X73832; NID:G435652; PIDN:CAA52054.1; PID:G435653
 A;Experimental source: type b, virulent strain Eagan
 C;Genetics:
 A;Gene: soda
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Superfamily: superoxide dismutase (Mn)
 C;Keywords: manganese; metalloprotein; oxidoreductase
 F:27,83,170,174/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.2%; Score 67; DB 2; Length 211;
 Best Local Similarity 44.4%; Pred. No. 0.015;
 Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAATEPYISQINEIXY 28
 DB 3 YTLPELGAYNALEPHFDAQTWEIHHS 29

RESULT 34
 B75415
 superoxide dismutase (EC 1.15.1.1) (Mn) DR1279 [similarity] - Deinococcus radiodurans (s
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
 C;Accession: B75415
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: B75415
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <WHI>
 A;Cross-references: GB:AE0001975; GB:AE000513; NID:G6459022; PIDN:AAFI0851.1; PID:G645902
 A;Experimental source: strain R1

C;Genetics:

A;Gene: DR1279

A;Map position: 1

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F:27,81,173,177/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

46.2%; Score 67; DB 2; Length 211;

Best Local Similarity 44.4%; Pred. No. 0.015;

Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAATEPYISQINEIXY 28

DB 3 YTLPELGAYNALEPHFDAQTWEIHHT 29

RESULT 35

C64182

superoxide dismutase (EC 1.15.1.1) (Mn) - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-May-2000

C;Accession: C64182

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: C64182

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-215 <TIGR>

A;Cross-references: GB:U32789; GB:L42023; NID:G1574642; PIDN:AAC22745.1; PID:G1574643; T

A;Experimental source: strain Rd KW20

C;Genetics:

A;Gene: soda

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F:27,83,170,174/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

46.2%; Score 67; DB 2; Length 215;

Best Local Similarity 44.4%; Pred. No. 0.015;

Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAATEPYISQINEIXY 28

DB 3 YTLPELGAYNALEPHFDAQTWEIHHS 29

RESULT 36

T50828

superoxide dismutase (EC 1.15.1.1) (Mn) 1 [similarity] - Prunus persica

C;Species: Prunus persica

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000

C;Accession: T50828

R;Bagnoli, F.

submitted to the EMBL Data Library, October 1999

A;Reference number: Z25247

A;Accession: T50828

A;Status: preliminary; translated from GB/EMBL/DBUJ

A;Molecule type: mRNA

A;Residues: 1-228 <BAG>

A;Cross-references: EMBL:AJ238316; PIDN:CAB56851.1

C;Genetics:

A;Gene: sod

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F:52,100,189,193/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

46.2%; Score 67; DB 2; Length 228;

Best Local Similarity 46.2%; Pred. No. 0.016;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEPYISGQINEIXY 27
DB 28 FSLPDLFYNYGALPAISGDMQLHH 53

RESULT 37
B48684
superoxide dismutase (EC 1.15.1.1) (Mn) 3-2 precursor - maize
C:Species: Zea mays (maize)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Apr-2000
C:Accession: B48684
R:Zhu, D.; Scandalios, J.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 9310-9314, 1993
A:Title: Maize mitochondrial manganese superoxide dismutases are encoded by a different
A:Reference number: A48684; MUID:94022365; PMID:8415698
A:Accession: B48684
A:Molecule type: mRNA
A:Residues: 1-233 <ZHU>
A:Cross-references: GB:119461
A:Experimental source: line W64A, embryos
A>Note: the authors translated the codon AGG for residue 143 as Lys and inserted an addi
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-29/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:57,105,194,198/Binding site: manganese (His, Asp, His) #status predicted

Query Match 46.2%; Score 67; DB 2; Length 233;
Best Local Similarity 48.0%; Pred. No. 0.017; 7; Indels 0; Gaps 0;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 SLPELDYEFSAPEPYISGQINEIXY 27
DB 34 ALPDLISYDFGALPAISGEIMRLHH 58

RESULT 38
S03839
superoxide dismutase (EC 1.15.1.1) (Mn) sod3 precursor [validated] - maize
C:Species: Zea mays (maize)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Apr-2000
C:Accession: S03839
R:White, J.A.; Scandalios, J.G.
Biochim. Biophys. Acta 951, 61-70, 1988
A:Title: Isolation and characterization of a cDNA for mitochondrial manganese superoxide
A:Reference number: S03839; MUID:89051020; PMID:2461225
A:Accession: S03839
A:Molecule type: mRNA
A:Residues: 1-235 <WHI>
A:Cross-references: EMBL:X12540
A:Experimental source: inbred line W64A
A>Note: 36-Ala was also found
A>Note: part of this sequence, including the amino end of the mature protein, was confir
A>Note: the authors translated the codon TTC for residue 154 as Leu
C:Genetics:
A:Gene: sod3
A:Genome: nuclear
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-31/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:32-235/Product: superoxide dismutase (Mn) #status experimental <MAN>
F:59,107,196,200/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 46.2%; Score 67; DB 2; Length 235;
Best Local Similarity 48.0%; Pred. No. 0.017;
Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 3 SLPELDYEFSAPEPYISGQINEIXY 27
DB 36 TLPDLISYDFGALPAISGEIMRLHH 60

RESULT 39
S53456
superoxide dismutase (EC 1.15.1.1) (Mn), 23K - maize (fragments)
C:Species: Zea mays (maize)
C>Date: 01-Aug-1995 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C:Accession: S53456
R:Feldwisch, J.; Zettl, R.; Campos, N.; Palme, K.
Biochem. J. 305, 853-857, 1995
A:Title: Identification of a 23 kDa protein from maize photoaffinity-labelled with 5-azi
A:Reference number: S53456; MUID:95151021; PMID:7848285
A:Accession: S53456
A:Molecule type: protein
A:Residues: 1-27; 28-43 <FEL>
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: metalloprotein; oxidoreductase

Query Match 45.5%; Score 66; DB 2; Length 43;
Best Local Similarity 60.0%; Pred. No. 0.0029;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 SLPELDYEFSAPEPYISGQI 22
DB 5 TLPDLISYDFGALPAISGEI 24

RESULT 40
AG0493
superoxide dismutase (EC 1.15.1.1) [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG0493
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0493
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC93515.1; PID:gi5981956; GSPDB:GN00175
C:Genetics:
A:Gene: soda
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: oxidoreductase

Query Match 45.5%; Score 66; DB 2; Length 207;
Best Local Similarity 48.1%; Pred. No. 0.02;
Matches 13; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 YSLPELDYEFSAPEPYISGQINEIXYT 28
DB 3 YSLPSLPYAYDALEPHFDKQTWEIHTT 29

Search completed: August 24, 2004, 23:03:46
Job time : 39 secs

